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OM nucleic - nucleic search, using sw model

Run on: December 18, 2004, 15:14:56 ; Search time 92.2085 Seconds  
(without alignments)  
7138.064 Million cell updates/sec

Title: US-09-996-529A-4

Perfect score: 926

Sequence: 1 gggggccattctgttcagc.....ttgatgtgtaaaaaaaaaa 926

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	926	100.0	926	US-09-561-497-3	Sequence 3, Appli
2	648	70.0	4793	US-09-561-497-10	Sequence 10, Appl
3	488.4	52.7	509	US-08-151-391A-1	Sequence 1, Appli
4	442.2	47.8	721	US-08-896-164-30	Sequence 30, Appl
5	440.8	47.6	502	US-08-151-391A-3	Sequence 3, Appli
6	341.6	36.9	461	US-08-896-164-31	Sequence 31, Appl
7	89	9.6	171	US-09-513-999C-13300	Sequence 13300, A
8	75	8.1	360	US-08-256-077-3	Sequence 3, Appli
9	75	8.1	360	US-08-466-127-3	Sequence 3, Appli
10	75	8.1	982	US-08-256-077-1	Sequence 1, Appli
11	75	8.1	982	US-08-466-127-1	Sequence 1, Appli
12	72	7.8	626	US-09-621-976-2005	Sequence 2005, Ap
13	50	5.4	432	US-08-642-255-48	Sequence 48, Appl
14	50	5.4	756	US-08-642-255-50	Sequence 50, Appl
15	47.8	5.2	969	US-09-252-991A-8086	Sequence 8086, Ap
16	47.8	5.2	1008	US-09-252-991A-8042	Sequence 8042, Ap
17	47.8	5.2	1194	US-09-252-991A-8227	Sequence 8227, Ap
18	46	5.0	1635	US-09-234-332-4	Sequence 4, Appli
19	46	5.0	1635	US-09-702-705-1798	Sequence 1798, Ap
20	46	5.0	1635	US-09-736-457-1798	Sequence 1798, Ap
21	46	5.0	1635	US-09-671-325-1798	Sequence 1798, Ap
22	46	5.0	1845	US-09-614-034-188	Sequence 188, App
23	46	5.0	23673	US-09-773-816-1	Sequence 1, Appli
24	45.4	4.9	6265	US-09-129-112-3	Sequence 3, Appli
25	43.6	4.7	485	PCT-US95-05741-10	Sequence 10, Appl
26	43.6	4.7	1309	US-08-362-495-4	Sequence 4, Appli
27	43.6	4.7	1309	US-09-408-508-4	Sequence 4, Appli

C	28	43.2	4.7	1992	4	US-09-252-991A-13771	Sequence 13771, A
	29	43.2	4.7	2175	4	US-09-252-991A-13657	Sequence 13657, A
	30	43.2	4.7	2292	4	US-09-252-991A-13575	Sequence 13575, A
	31	42.4	4.6	837	4	US-09-252-991A-4221	Sequence 4221, Ap
C	32	42.4	4.6	1080	4	US-09-252-991A-4664	Sequence 4664, Ap
	33	42.4	4.6	1268	4	US-09-475-515-9	Sequence 9, Appli
	34	42.4	4.6	1299	4	US-09-252-991A-11249	Sequence 11249, A
	35	42.4	4.6	1515	4	US-09-475-515-4	Sequence 4, Appli
C	36	42.4	4.6	1537	4	US-09-252-991A-11008	Sequence 11008, A
	37	42.4	4.6	1806	4	US-10-140-002-121	Sequence 121, App
	38	42.4	4.6	1853	4	US-09-475-515-5	Sequence 5, Appli
	39	42.4	4.6	1865	4	US-09-475-515-78	Sequence 78, Appl
	40	42.4	4.6	1865	4	US-09-475-515-79	Sequence 79, Appl
	41	42.4	4.6	2031	4	US-09-475-515-7	Sequence 7, Appli
	42	42.4	4.6	4319	4	US-09-475-515-6	Sequence 6, Appli
	43	42.4	4.6	4472	4	US-09-475-515-75	Sequence 75, Appl
	44	42.4	4.6	4608	4	US-09-475-515-76	Sequence 76, Appl
	45	42.4	4.6	4689	4	US-09-475-515-74	Sequence 74, Appl

#### ALIGNMENTS

RESULT 1  
US-09-561-497-3

Sequence 3, Application US/09561497  
Patent No. 6372433

GENERAL INFORMATION:

APPLICANT: Brenda F. Baker

APPLICANT: C. Frank Bennett

APPLICANT: Jacqueline Warr

TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR OF DNA BINDING-1 EXPRESSION

FILE REFERENCE: RTS-0149

CURRENT APPLICATION NUMBER: US/09/561,497

CURRENT FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 88

SEQ ID NO 3

LENGTH: 926

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (36)...(500)

US-09-561-497-3

Query Match 100.0%; Score 926; DB 3; Length 926;  
Best Local Similarity 100.0%; Pred. No. 5.8e-240;  
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GGGGCCATTCTGTTTCAGCCAGTCCCAAGATATGAAAGTCCCAAGACACCG	60
DB	1	GGGGCCATTCTGTTTCAGCCAGTCCCAAGATATGAAAGTCCCAAGTGCACACG	60
QY	61	CCACCGCCGCGCGCGCGCGCGCGCGCTGAAGCGCGCGCAAGACAGCGGTGCGG	120
DB	61	CCACCGCCGCGCGCGCGCGCGCGCGCTGAAGCGCGCGCAAGACAGCGGTGCGG	120
QY	121	GGAGGTGTGCGGTGTGTGTGTCAGACAGAGCGTGCATCTGCGGTCCGCGGCGCG	180
DB	121	GGAGGTGTGCGGTGTGTGTGTCAGACAGAGCGTGCATCTGCGGTCCGCGGCGCG	180
QY	181	GGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240
DB	181	GGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	240
QY	241	ACGGCTGTATCTACGCGCTCAAGAGCGTGTGCCACCTGCCAGAACGCAAGTGA	300
DB	241	ACGGCTGTATCTACGCGCTCAAGAGCGTGTGCCACCTGCCAGAACGCAAGTGA	300
QY	301	GCAAGTGTGAGATTCTCCAGACGTCATCGATCATCATCAGGAGACCTTCAGTTGAGCTGA	360
DB	301	GCAAGTGTGAGATTCTCCAGACGTCATCGATCATCATCAGGAGACCTTCAGTTGAGCTGA	360

QY 361 ACTCGGAATCCGAAGTTGGAGACCCCGGAGGAGCCGAGTCCGGCTCCGGCTCA 420  
 Db 361 ACTCGGAATCCGAAGTTGGAGACCCCGGAGGAGCCGAGTCCGGCTCCGGCTCA 420  
 QY 421 GCACCCCTCAACGGCGCAGATCAAGCGCCCTGAGAGGCGCAGAGCGGCAATGCGTTCTGCGGACG 480  
 Db 421 GCACCCCTCAACGGCGCAGATCAAGCGCCCTGAGAGGCGCAGAGCGGCAATGCGTTCTGCGGACG 480  
 QY 481 ATCGCATTTTGTGTGCTGAGAGCGCTTCCCGCAGGAGACCGGCGGACCCCGCATCCGAG 540  
 Db 481 ATCGCATTTTGTGTGCTGAGAGCGCTTCCCGCAGGAGACCGGCGGACCCCGCATCCGAG 540  
 QY 541 GGGCAGAGGAATTAACGTGCTGTGGAGTCTCCCCCAACGCGCTCGCGCATCTGAAGG 600  
 Db 541 GGGCAGAGGAATTAACGTGCTGTGGAGTCTCCCCCAACGCGCTCGCGCATCTGAAGG 600  
 QY 601 AGAACAAAGACCGATCGCGCGCACTGCGCCCTTAACTGCATCCAGCCTGGGGCTGAGGCT 660  
 Db 601 AGAACAAAGACCGATCGCGCGCACTGCGCCCTTAACTGCATCCAGCCTGGGGCTGAGGCT 660  
 QY 661 GAGGCACTGCGCAGAGAGAGGCGCTCTCTGACCAACCACTAATGTCACCAAGACTTTA 720  
 Db 661 GAGGCACTGCGCAGAGAGAGGCGCTCTCTCTGACCAACCACTAATGTCACCAAGACTTTA 720  
 QY 721 GGGGGTGGGATTCACCTCGTGTGTTCTAATTTTTGAAAGCAGACATTTTAAAAATGG 780  
 Db 721 GGGGGTGGGATTCACCTCGTGTGTTCTAATTTTTGAAAGCAGACATTTTAAAAATGG 780  
 QY 781 TCACGTTGGTGTCTTCAGATTCCTGAGGAAATGCTTGTATGTATTAACAATGAT 840  
 Db 781 TCACGTTGGTGTCTTCAGATTCCTGAGGAAATGCTTGTATGTATTAACAATGAT 840  
 QY 841 CACCGCATGAGATATGTTTTCAAATAGTTCCTGAGGCGCTGTTTTTGTATTAACA 900  
 Db 841 CACCGCATGAGATATGTTTTCAAATAGTTCCTGAGGCGCTGTTTTTGTATTAACA 900  
 QY 901 AATAATTAGATGTGAAAAAAAAA 926  
 Db 901 AATAATTAGATGTGAAAAAAAAA 926  
 RESULT 2  
 US-09-561-497-10  
 / Sequence 10, Application US/09561497  
 / Patent No. 6372433  
 / GENERAL INFORMATION:  
 / APPLICANT: Brenda F. Baker  
 / APPLICANT: C. Frank Bennett  
 / APPLICANT: Jacqueline Wyatt  
 / TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR OF DNA BINDING-1 EXPRESSION  
 / FILE REFERENCE: RTS-0149  
 / CURRENT APPLICATION NUMBER: US/09/561,497  
 / CURRENT FILING DATE: 2000-04-28  
 / NUMBER OF SEQ ID NOS: 86  
 / SEQ ID NO 10  
 / LENGTH: 4793  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 / FEATURE:  
 / NAME/KEY: CDS  
 / LOCATION: (2210) ... (2659)  
 / US-09-561-497-10

Query Match	70.0%	Score 648	DB 3	Length 4793
Best Local Similarity	78.7%	Pred. No. 1.3e-164		
Matches 913	Conservative	0	Mismatches 5	Indels 242
Gaps				
QY	4	GCCCATCTCTGTTTCAGCCAGTCGCCAAGAATCATGAAGTCGCACTGCACACCGCA	63	
Db	2178	GCCCATCTCTGTTTCAGCCAGTCGCCAAGAATCATGAAGTCGCACTGCACACCGCA	2237	
QY	64	CCGCGCGCGCGGAGCCCAAGTCGCGCTGAAGCCGCAAGACGCGAGCGTGGGCG	123	

D	2238	CCGCCCGCGGAGCCCGAGCTGCGCGCTGAAGGCCCGGCAAGACAGCGCGGTGCGGGC	2297
Q	124	AGGTGTGCGCTGTCTGTCTGAGCAGAGCGTGCCCATCTCCGGCTG---CCGGGCGCG	180
D	2298	AGGTGTGCGCTGTCTGTCTGTGACAGAGCGTGCCCATCTCGGCGCGCGCGGGCGCGC	2357
Q	181	GGGGCGCGCTGCTGCTGCTGTGAGCAGACAGAGTAAACGTGTGCTTACGACATGA	240
D	2358	GGGGCGCGCTGCGCTGCTGTGAGCAGACAGAGTAAAGTGTGCTTACGACATGA	2417
Q	241	ACGGCTTTACTACGCGCTCAAGGAGCCTGTGCCCCACCTCTGCCAAGCGCAAGTGA	300
D	2418	ACGGCTTTACTACCGCTCTCAGAGAGCTGTGCCCCACCTCTGCCAAGCGCAAGTGA	2477
Q	301	GCAAGGTGAGATTTCTCCAGACGTCATCGACTACATCAGGAGACCTTCAGTTGAGCTGA	360
D	2478	GCAAGGTGAGATTTCTCCAGACGTCATCGACTACATCAGGAGACCTTCAGTTGAGCTGA	2537
Q	361	ACTCGGAATCCGAAGTTGGGGAACCCCGGGGGCCGAGGGCTGCCGATCCGATCCGCTCA	420
D	2538	ACTCGGAATCCGAAGTTGGGGAACCCCGGGGGCCGAGGGCTGCCGATCCGATCCGCTCA	2597
Q	421	GCACTCTCAACGCGCAGATCAGCGGCTCGACGGCG-----	456
D	2598	GCACTCTCAACGCGCAGATCAGCGGCTCGACGGCGCGAGTGAATCCAGTCGACCACT	2657
Q	457	-----	456
D	2658	AGATCATCTTATACCGACGCGGAAACGAGAGCCAGAGAGGCGTGCGCTTGACACAC	2717
Q	457	-----	456
D	2718	TTCCGTCCTCTTGGCGGATCCTGCGCTATCGCGGGTCTCTAAGAGCTGGAATAAG	2777
Q	457	-----	456
D	2778	CGCTCCCCGTCGTGCTTCTGAGGAAAGGGCGTTGCTGCGCTCGAGCGCGCTCT	2837
Q	457	-----AGCGGCACTGCGTTCTCTGCGACGA	481
D	2838	TCGAACCCCGCGGTCTCATTTCTTCTGTTTCAACAGGGCGGCAATGGGTTCTGCGAGCA	2897
Q	482	TGCACTTGTGTGCTGAAGCGCTTCCCGCAGAGACCGCGGACCCGACCATCGAGG	541
D	2898	TGCACTTGTGTGCTGAAGCGCTTCCCGCAGAGACCGCGGACCCGACCATCGAGG	2957
Q	542	GCGAAGAGGAATTAACGTGCTGTGGGTCTCCCCCAACGCGCTGCGCGATCTGAGGA	601
D	2958	GCGAAGAGGAATTAACGTGCTGTGGGTCTCCCCCAACGCGCTGCGCGATCTGAGGA	3017
Q	602	GAACAAAGCCGATCGCGGCGCACTGCGGCTTAACTGCATCCAGCCTGAGGCTGAGGTG	661
D	3018	GAACAAAGCCGATCGCGGCGCACTGCGGCTTAACTGCATCCAGCCTGAGGCTGAGGTG	3077
Q	662	AGGACGTGGAGAGAGAGGGCGCTCTCTCTGCACACTTACTGATCACCAGAGCTTTAG	721
D	3078	AGGACGTGGAGAGAGAGGGCGCTCTCTCTGCACACTTACTGATCACCAGAGCTTTAG	3137
Q	722	GGGCTGGATTCACCTGCTGTGTTCTATTTTGAAGAGACATTTTAAAAATGCT	781
D	3138	GGGCTGGATTCACCTGCTGTGTTCTATTTTGAAGAGACATTTTAAAAATGCT	3197
Q	782	CAGCTTGGTCTTCTCAGATTTCTGAGAAATGCTTTGTATGTATTAACAATGATC	841
D	3198	CAGCTTGGTCTTCTCAGATTTCTGAGAAATGCTTTGTATGTATTAACAATGATC	3257
Q	842	ACGCACTGAGAAATTTGTTTACAATTAATCTGTGCGGCGCTTTTTTGTATTAACA	901
D	3258	ACGCACTGAGAAATTTGTTTACAATTAATCTGTGCGGCGCTTTTTTGTATTAACA	3317
Q	902	ATAATTTAGATGCTGAATAA 921	
D	3318	ATAATTTAGATGCTGAATAA 3337	

RESULT 3  
US-08-151-391A-1  
; Sequence 1, Application US/08151391A  
; Patent No. 5527897  
; GENERAL INFORMATION:  
; APPLICANT: Oda, Kinichiro  
; APPLICANT: Nakada, Susumu  
; APPLICANT: Hara, Eiji  
; APPLICANT: Yamaguchi, Tomoko  
; APPLICANT: Nakamura, Takeshi  
; APPLICANT: Oka, Yumiko  
; APPLICANT: Kishimoto, Toshihiko  
; TITLE OF INVENTION: Human ID Genes  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER  
; STREET: 99 Canal Center Plaza, Suite 300  
; CITY: Alexandria  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/151,391A  
; FILING DATE: 12-NOV-1993  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Willis, Demetra J.  
; REGISTRATION NUMBER: 34,506  
; REFERENCE/DOCKET NUMBER: 715-087  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 684-1111  
; TELEFAX: (703) 684-1124  
; TELEX: 82-4425  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 509 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 22..483  
; OTHER INFORMATION: /note="CDS"  
US-08-151-391A-1  
Query Match 52.7%; Score 488.4; DB 1; Length 509;  
Best Local Similarity 98.6%; Pred. No. 4.3e-122;  
Matches 503; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 195 GCCCTGCTGAGCGACGACGAGTAAGCTGCTCTACGACATGACCGGCTGTACTCA 254  
DB 181 GCCCTGCTGAGCGACGACGAGTAAGCTGCTCTCTACGACATGACCGGCTGTACTCA 240  
QY 255 GCCTCAAGAGAGCTGTGTCGCCACCTGTCGCCAGAACCGCAAGGTAGAGAGATT 314  
DB 241 GCCTCAAGAGAGCTGTGTCGCCACCTGTCGCCAGAACCGCAAGGTAGAGATT 300  
QY 315 CTCACGACGCTGATGACTACATCAAGGACCTTCACTGTTGAGCTGAATCCGAA 374  
DB 301 CTCACGACGCTGATGACTACATCAAGGACCTTCACTGTTGAGCTGAATCCGAA 360  
QY 375 GTTGGAGACCCCGGGGGGCGAGGGCTGCGGATCCGCTCAGACCTCAAGCGC 434  
DB 361 GTTGGAGACCCCGGGGGGCGAGGGCTGCGGATCCGCTCAGACCTCAAGCGC 420  
QY 435 GAGATCAGCGCCCTGACCGCCGAGCGGATGCGTTCTGCGGACGATCGATCTTGCT 494  
DB 421 GAGATCAGCGCCCTGACCGCCGAGCGGATGCGTTCTGCGGACGATCGATCTTGCT 480  
QY 495 CGCTGAGCGCTCTCCCGCAGGAGCCGCGG 524  
DB 481 CGCTGAGCGCTCTCCCGCAGGAGCCGCGG 509

RESULT 4  
US-08-896-164-30  
; Sequence 30, Application US/08896164  
; Patent No. 6218521  
; GENERAL INFORMATION:  
; APPLICANT: OBATA, Yuichi  
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED  
; TITLE OF INVENTION: WITH GASTRIC CANCER AND METHODS FOR  
; TITLE OF INVENTION: DIAGNOSING AND TREATING GASTRIC CANCER  
; NUMBER OF SEQUENCES: 87  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Felfe & Lynch  
; STREET: 805 Third Avenue  
; CITY: New York City  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: PC-DOS  
; SOFTWARE: Wordperfect  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/896,164  
; FILING DATE: July 17, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 6218521man D. Hanson  
; REGISTRATION NUMBER: 30,946  
; REFERENCE/DOCKET NUMBER: LUD 5499 - JEL/NDH/SLH  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 688-9200  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 721 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-896-164-30  
Query Match 47.8%; Score 442.2; DB 3; Length 721;  
Best Local Similarity 95.1%; Pred. No. 1.5e-109;  
Matches 466; Conservative 0; Mismatches 21; Indels 3; Gaps 1;





CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/896,164  
FILING DATE: July 17, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6218521man D. Hanson  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5499 - JEL/NDH/SLH  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 461 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-896-164-31

Query Match 36.9%; Score 341.6; DB 3; Length 461;  
Best Local Similarity 79.3%; Pred. No. 1.6e-82;  
Matches 365; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 457 AGGCGCATGCGCTTCTGCGGAGATCGCATCTGTGCTGAAGCGCCCTCCCGAGG 516  
DB 461 AGCGCGCANGGCTTCTGCGGAGATCTGTGCTGAAGCGCCCTCCCGAGG 402  
QY 517 ACCGGCGGAGCCCGAGCCATCCAGGGGGCAAGAGATTACGTCTGTGGGTCTCCCG 576  
DB 401 ACCGGCGGAGCCCGAGCCATCCAGGGGGCAAGAGATTACGTCTGTGGGTCTCCCG 342  
QY 577 AACGGCGCTCCCGAGCTCTGAGGAGAACAGACCGATCGGGGCGCATCGCCCTTAC 636  
DB 341 NAAAGGCCCTGGCGGATTTGGGAGGAGNAGNCCGATTGGCGCAATGAGCCCTTAA 282  
QY 637 TGCATCCAGCGCTGAGGCTGAGGCTGAGGCTGAGGAGGAGGCGCTCTCTGCAC 696  
DB 281 TGNATNCGAGCTGGGGGNTGNGTGAAGCAATGAGGAGGAGGAGGAGGAGGAGGAG 222  
QY 697 ACCTAAGTACCAAGAGCTTTAAGGGGGTGGGATTCACCTGTGTGTTCTATTGTTG 756  
DB 221 ACCTAATAGTACCAAGAGATTTAAGGGGGTGGGATTCACCTGTGTGTTCTATTGTTG 162  
QY 757 AAAAGCAGACATTTTAAAAAATGTCACGTTTGTGCTTCTCAATTTCTGAGAAATTG 816  
DB 161 NAAAGCAGAAATTTTAAAAAATGTCACGTTTGTGCTTCTCAATTTCTGAGAAATTG 102  
QY 817 CTTTGTATGTATTTTAAATGATGACCGAGCTGAGATTTGTTTAAATGTTCTGTG 876  
DB 101 NTTTGTATTTTAAATGATGATGACCGAGTGAATATTTGTTTAAATGTTTGTG 42  
QY 877 GGGCTGTTTTTTTGTATTAAACAATATTAGATGTG 916  
DB 41 GGGGTGTTTTTTTGTATTAAANATATTAGTGTG 2

RESULT 7  
US-09-513-999C-13300  
Sequence 13300, Application US/09513999C  
GENERAL INFORMATION:  
APPLICANT: Dumas Maline Edwards, J.B.  
APPLICANT: Duclet, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6783961  
FILE REFERENCE: 59, US2, REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent. pm

SEQ ID NO 13300  
LENGTH: 171  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-513-999C-13300

Query Match 9.6%; Score 89; DB 4; Length 171;  
Best Local Similarity 99.0%; Pred. No. 1.2e-14;  
Matches 100; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 4 GCCATTCTGTTTACGACGAGTCCGCAAGATCATGAAGTCCGAGTGGACGACCGCA 63  
DB 72 GCCATTCTGTTTACGACGAGTCCGCAAGATCATGAAGTCCGAGTGGACGACCGCA 131  
QY 64 CCG 104  
DB 132 CCG 171

## RESULT 8

US-08-256-077-3  
Sequence 3, Application US/08256077  
Patent No. 5654188

GENERAL INFORMATION:  
APPLICANT: Weith, Andreas  
TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,077  
FILING DATE: 23-JUNE-1994

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 0652.1360000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 360 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-256-077-3

Query Match 8.1%; Score 75; DB 1; Length 360;  
Best Local Similarity 58.0%; Pred. No. 1.1e-10;  
Matches 163; Conservative 0; Mismatches 100; Indels 18; Gaps 1;

QY 91 TGAAGCGCGGAG 150  
DB 2 TGAAGCGCGGAG 61  
QY 151 GCGTGGCATCTCGCGCTGCGGGGCGCGGGGCGCGGCTGCTGCTGAGAGAGC 210  
DB 62 GCTGGCCATCGCGCGGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 118  
QY 211 AGCAGTAAAGTGTGTCTACAGACATGAACGAGCTGTACTCAGGCTCAAGAGAGCTGG 270

Db 119 -----TCTGAGACGATGAACCACTGCTACTCCGCTGGCGGAATCG 163  
QY 271 TGCCCACTCCCGCAGAACCGCAAGGTGAGAGATTCTCCAGCAGTATCG 330  
Db 164 TACCCGAGATCCGAGAGGACCTAGCTTAGCCAGGTGGAATCTTACAGCGGTATCG 223  
QY 331 ACTACATCAGGACCTTCACTGAGAGTGAATCTCGGAATCC 371  
Db 224 ACTACATCTCGACCTCGAGGTAGTCTTGGCCGAGCAGCC 264

RESULT 9  
US-08-466-127-3  
; Sequence 3, Application US/08466127  
; Patent No. 5683878  
; GENERAL INFORMATION:  
; APPLICANT: Elimeier, Wilfried  
; TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,127  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 0652.1360002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 360 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; NAME/KEY: CDS  
; LOCATION: 1..357  
; US-08-466-127-3

Query Match 8.1%; Score 75; DB 1; Length 360;  
Best Local Similarity 58.0%; Pred. No. 1.1e-10;  
Matches 163; Conservative 0; Mismatches 100; Indels 18; Gaps 1;

Db 164 TACCCGAGATCCCGAGAGGACCTAGCTTAGCCAGGTGGAATCTTACAGCGGTATCG 223  
QY 331 ACTACATCAGGACCTTCACTGAGAGTGAATCTCGGAATCC 371  
Db 224 ACTACATCTCGACCTCGAGGTAGTCTTGGCCGAGCAGCC 264

RESULT 10  
US-08-256-077-1  
; Sequence 1, Application US/08256077  
; Patent No. 5654188  
; GENERAL INFORMATION:  
; APPLICANT: Elimeier, Wilfried  
; TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,077  
; FILING DATE: 23-JUNE-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 0652.1360000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 982 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; US-08-256-077-1

Query Match 8.1%; Score 75; DB 1; Length 982;  
Best Local Similarity 58.0%; Pred. No. 1.8e-10;  
Matches 163; Conservative 0; Mismatches 100; Indels 18; Gaps 1;

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RESULT 11
US-08-466-127-1
; Sequence 1, Application US/08466127
; Patent No. 5683878
; GENERAL INFORMATION:
; APPLICANT: Eilmeler, Wilfried
; APPLICANT: Weith, Andreas
; TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,127
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 0652.1360002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 982 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 37..481
; US-08-466-127-1

Query Match      8.1%; Score 75; DB 1; Length 982;
Best Local Similarity 58.0%; Pred. No. 1.8e-10;
Matches 163; Conservative 0; Mismatches 100; Indels 18; Gaps 1;
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; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Mline Edwards, J.B.
; APPLICANT: Jodert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2005
; LENGTH: 626
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 211..570
; NAME/KEY: sig_peptide
; LOCATION: 211..378
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 3.5999990463257
; OTHER INFORMATION: seq LOIAGLXPLX/DL
US-09-621-976-2005
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Query Match      7.8%; Score 72; DB 4; Length 626;
Best Local Similarity 77.9%; Pred. No. 9.3e-10;
Matches 95; Conservative 3; Mismatches 23; Indels 1; Gaps 1;

QY 227 GCTTACGACATGAGCGGCTGTACTCAGCGCTCAAGAGGTGTGCCACCTGCCCA 286
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DB 220 KSTATACACATGAAGCACTCTCTCAAGCTCAAGAGGTGTGCCACATCCCCA 279
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QY 287 GAACCGCAAGGTGAGCAAGGTGAGATTCTCCAGACGT-CATGACTTACATCAGGACC 345
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DB 280 GACCAAGAGGTGAGCAAGATGAAATCTCGACAGACGTCAATGACTATCTTGGGAC 339
    |||

QY 346 TT 347
DB 340 CT 341

RESULT 13
US-08-642-255-48
; Sequence 48, Application US/08642255
; Patent No. 5773249
; GENERAL INFORMATION:
; APPLICANT: CAPPELLO, Joseph A.
; APPLICANT: FERRARI, Franco A.
; TITLE OF INVENTION: High Molecular Weight Collagen-Like
; TITLE OF INVENTION: Protein Polymers
; NUMBER OF SEQUENCES: 135
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,255
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ROWLAND, Bertram I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A55556-3/BIR
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (415) 494-8700  
TELEFAX: (415) 494-8771  
TELEX: 910 277299 FRT UR  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 432 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic"  
US-08-642-255-48

Query Match 5.4%; Score 50; DB 1; Length 432;  
Best Local Similarity 50.0%; Pred. No. 0.00066;  
Matches 152; Conservative 0; Mismatches 150; Indels 2; Gaps 1;

QY 51 GGCAGCACCGCCACCGCCGCGCGGCCCAAGCTGCGGCTGAAGCGCGGCAAGACAGCG 110  
DB 123 GGCCTGCTCCACCGGGTCTCCGGGACCTGCAAGGCCCGCCAGGTGGCTGACCGGCTGG 182  
QY 111 AGCGGTGCGGCGGAGGTGCTGCTGTCTGAGCAGAGCGTGGCCATTCGGGCTGC 170  
DB 183 TCCACCGGGTCTCCGGGACCTGCAAGGCCCGCCAGGTGGCTGACCGGCTGTCCACC 242  
QY 171 CGGGGCGCGGGGCGCGGCTGCTGCC--CTGCTGAGCAGCAGAGGTAACGTGCTGC 228  
DB 243 GGGTCTCCGGGACCTGCAAGGCCCGCCAGGTGGCTGGAACGGCTGTCCACCGGCTGC 302  
QY 229 TCTACGACATGAACGGCTGTACTCAAGCTCAAGAGAGTGTGGCCACCCTGCCCCAGA 288  
DB 303 TCCGGGACCTGCAAGGCCCGCCAGGTGGCTGGAACGGCTGTCCACCGGCTGTCCGGG 362  
QY 289 ACCGCAAGTGAAGAGTGAATTTCCAGCAGCTGATGACTACATCAGGAGCTTC 348  
DB 363 ACCGCAAGGCCCGCCAGGTGGCTGCAAGGCCCGCCAGAGACGAAAGAGCTCACGGTCCGGC 422  
QY 349 AGTT 352  
DB 423 AGGT 426

RESULT 14  
US-08-642-255-50  
Sequence 50, Application US/08642255  
Patent No. 5773249  
GENERAL INFORMATION:  
APPLICANT: CAPPELO, Joseph  
APPLICANT: FERRARI, Franco A.  
TITLE OF INVENTION: High Molecular Weight Collagen-Like  
TITLE OF INVENTION: Protein Polymers  
NUMBER OF SEQUENCES: 135  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FLEHR, HOEBACH, TEST, ALABRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-4187  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/642,255  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: ROWLAND, Bertram I.  
REGISTRATION NUMBER: 20,015  
REFERENCE/DOCKET NUMBER: A5556-3/BIR  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 494-8700  
TELEFAX: (415) 494-8771  
TELEX: 910 277299 FRT UR  
INFORMATION FOR SEQ ID NO: 50:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 756 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic"  
US-08-642-255-50

Query Match 5.4%; Score 50; DB 1; Length 756;  
Best Local Similarity 50.0%; Pred. No. 0.00088;  
Matches 152; Conservative 0; Mismatches 150; Indels 2; Gaps 1;

QY 51 GGCAGCACCGCCACCGCCGCGGCGGCCCAAGCTGCGGCTGAAGCGCGGCAAGACAGCG 110  
DB 447 GGCCTGCTCCACCGGGTCTCCGGGACCTGCAAGGCCCGCCAGGTGGCTGACCGGCTGG 506  
QY 111 AGCGGTGCGGCGGAGGTGCTGCTGTCTGAGCAGAGCGTGGCCATTCGGGCTGC 170  
DB 507 TCCACCGGGTCTCCGGGACCTGCAAGGCCCGCCAGGTGGCTGACCGGCTGTCCACC 566  
QY 171 CGGGGCGCGGGGCGCGGCTGCTGCC--CTGCTGAGCAGCAGAGGTAACGTGCTGC 228  
DB 567 GGGTCTCCGGGACCTGCAAGGCCCGCCAGGTGGCTGGAACGGCTGTCCACCGGCTGC 626  
QY 229 TCTACGACATGAACGGCTGTACTCAAGCTCAAGAGAGTGTGGCCACCCTGCCCCAGA 288  
DB 627 TCCGGGACCTGCAAGGCCCGCCAGGTGGCTGGAACGGCTGTCCACCGGCTGTCCGGG 686  
QY 289 ACCGCAAGTGAAGAGTGAATTTCCAGCAGCTGATGACTACATCAGGAGCTTC 348  
DB 687 ACCGCAAGGCCCGCCAGGTGGCTGCAAGGCCCGCCAGAGACGAAAGAGCTCACGGTCCGGC 746  
QY 349 AGTT 352  
DB 747 AGGT 750

RESULT 15  
US-09-252-991A-8086  
Sequence 8086, Application US/09252991A  
Patent No. 6531795  
GENERAL INFORMATION:  
APPLICANT: MARC J. RUBENFIELD et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196,136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 8086  
LENGTH: 969  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-8086

Query Match 5.2%; Score 47.8; DB 4; Length 969;  
Best Local Similarity 46.5%; Pred. No. 0.0039;  
Matches 154; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

QY 33 ATCATGAAAGTCCGCTGAGCAGACCGCCGCGGCGGCCCGCCAGCTGCGGCTG 92  
DB 163 ATGAAAGAACTCCCGCCATCAACCGGCTGCTGCTGATTCGCGGCTGAGCCAG 222  
QY 93 AAGCGCGGCAAGACAGAGCGGTGGCGGGGAGAGTGTGCTGTCTGAGCAGAGC 152

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Db      223  GCCGACCGGCTGGAGGACATCCGCAAGGCCGGCGTATTGCGGTGCGGCTTCCTTCACAGC 282
QY      153  GTGGCAATCTCGCGCTGCGGGGGCGCCGGGGCGCGCTGCTGCCCTGCTGGACGACAG 212
Db      283  AACCGCGGTTTCGGCTTCGTGACGCCCAAGACAGATCGAAGGCTTCGACGCTCGAC 342
QY      213  CAGGTAAAGTGTGCTGCTCTAGACATGAAAGGCTGTTACTCAGGCTCAAGGAGCTGGTG 272
Db      343  TATGCCAAGGCCCTTGCGGACCAAGCTGGGCGTCCGGCTGCAGTGTGCGGACCAACCG 402
QY      273  CCCACCTTGCCCGCAGAACCGCAAGGTGACAGATTCCTCCAGCACGTCATCGAC 332
Db      403  GCCAACCGGATCCGCTGTGTGACGGGAAAGAGTGAAGTGTGCTGCTGCGCAACTTCACC 462
QY      333  TACATCAGGAGCTTCAGTTGAGCTGAAGT 363
Db      463  ATCACCCTCGGAGCGTGCAGCAGGTGGACT 493
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Search completed: December 18, 2004, 20:46:21  
Job time : 96.2085 secs

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Db	181	GGGGGCGCCTCCGTCCTGCTGACGAGCAGGAGTAAACGTCCTCTCTACGACATGA	240
Qy	241	ACGCGCTGTACTCA CGCCTCAAGGAGCTGAGCCACCTCGGCCAGAAACGGAAGGTGA	300
Db	241	ACGCGCTGTACTCA CGCCTCAAGGAGCTGAGGCCACCTCGGCCAGAAACGGAAGGTGA	300
Qy	301	GCAAGGTGAGAGATTCTCAGACAGCTCAATCCACTATCATCAGGAGCTTCA GTTGAAGCTGA	360
Db	301	GCAAGGTGAGAGATTCTCAGACAGCTCAATCCACTATCATCAGGAGCTTCA GTTGAAGCTGA	360
Qy	361	ACTCGGAATCCGAAGTTGGGACCCCGCGGGGACGAGGGGCTGCGGAGTCCCGCTCA	420
Db	361	ACTCGGAATCCGAAGTTGGGACCCCGCGGGGACGAGGGGCTGCGGAGTCCCGCTCA	420
Qy	421	GCACCCCTCAACGGGAGATATCAGGCGCCCTGA CGGCGGAGGTGGCATATGCTTCTGCGGACG	480
Db	421	GCACCCCTCAACGGGAGATATCAGGCGCCCTGA CGGCGGAGGTGGCATATGCTTCTGCGGACG	480
Qy	481	ATTCGATCTTGTGTGCTGAGAGCGCTCCGCCAGGACCGGCGGAGCCCGACGCATCCAG	540
Db	481	ATTCGATCTTGTGTGCTGAGAGCGCTCCGCCAGGACCGGCGGAGCCCGACGCATCCAG	540
Qy	541	GGGCAAGAGGAATTACGTGCTCTGTGGAGTCTCCCCAAGCGGCTGCGCGAATTGAGGG	600
Db	541	GGGCAAGAGGAATTACGTGCTCTGTGGAGTCTCCCCAAGCGGCTGCGCGAATTGAGGG	600
Qy	601	AGAACAAAGACCGATCGGCGGCGCACTCGGCCCTTAACTGATCAGGCTGGGGCTAGAGCT	660
Db	601	AGAACAAAGACCGATCGGCGGCGCACTCGGCCCTTAACTGATCAGGCTGGGGCTAGAGCT	660
Qy	661	GAGGCACTGGCCAGAGAGAGGGCGGCTCTCTCTGACACCTTACTAGTACACAGACTTTA	720
Db	661	GAGGCACTGGCCAGAGAGAGGGCGGCTCTCTCTGACACCTTACTAGTACACAGACTTTA	720
Qy	721	GGGGGTGGGATTCACCTCGTGTGTTCTAATTTTGGAAAGCAGACATTTTAAAAAATGG	780
Db	721	GGGGGTGGGATTCACCTCGTGTGTTCTAATTTTGGAAAGCAGACATTTTAAAAAATGG	780
Qy	781	TCACGTTGGTGTCTCTCAGATTTCTGAGAAATTGCTTTGTAATGTATATTAACAATGAT	840
Db	781	TCACGTTGGTGTCTCTCAGATTTCTGAGAAATTGCTTTGTAATGTATATTAACAATGAT	840
Qy	841	CACCGACTGAGAAATATTTGTTTACAAATAGTATCTGAGGGGCTTTTTTGTATTAACA	900
Db	841	CACCGACTGAGAAATATTTGTTTACAAATAGTATCTGAGGGGCTTTTTTGTATTAACA	900
Qy	901	AATATTTAGATGTGTAACAAAAA 926	
Db	901	AATATTTAGATGTGTAACAAAAA 926	

RESULT 2				
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LOCUS	AR206583			
DEFINITION	Sequence 3	926 bp	DNA	linear
ACCESSION	AR206583			PAT 20-JUN-2002
VERSION	AR206583.1			
KEYWORDS	GI:21505231			
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 926)			
TITLE	Baker, B.F., Bennett, C. Frank, and Wyatt, J.			
JOURNAL	Antisense modulation of inhibitor of DNA binding-1 expression			
FEATURES	Patent: US 6372433-A 3 16-APR-2002;			
source	Location/Qualifiers			
	1..926			

ORIGIN	/mol_type="unassigned DNA"
Query Match	100.0%; Score 926; DB 6; Length 926
Best Local Similarity	100.0%; P-Id. No. 8; 8e-174;

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QY	1	GGGGCCCATTC	CTGTTTCAGCC	CAGTCCG	CCAAAGATCAT	TAAAGATCG	CCAGTGG	CACACCG	60	
Db	1	GGGGCCCATTC	CTGTTTCAGCC	CAGTCCG	CCAAAGATCAT	TAAAGATCG	CCAGTGG	CACACCG	60	
QY	61	CCACCCGCGCG	CGGGGCCCA	GTGCGCCT	GAAGCGCGG	CAGACAG	CGCGTGG	120		
Db	61	CCACCCGCGCG	CGGGGCCCA	GTGCGCCT	GAAGCGCGG	CAGACAG	CGCGTGG	120		
QY	121	GCAGAGTGG	ACGCTGTC	GTGAGCAG	AAGGTGGCCAT	CTCGGCTG	CCGGGCGCG	180		
Db	121	GCAGAGTGG	ACGCTGTC	GTGAGCAG	AAGGTGGCCAT	CTCGGCTG	CCGGGCGCG	180		
QY	181	GGGCGCGCCT	GCTGCTG	CTGAGCAG	AGGTAAAGT	GTGCTCTA	GCAGCATGA	240		
Db	181	GGGCGCGCCT	GCTGCTG	CTGAGCAG	AGGTAAAGT	GTGCTCTA	GCAGCATGA	240		
QY	241	ACGGCTGTTA	CTCAGCCTC	CAAGAGCT	GTGGCCACCT	TGCGCAG	ACCGAAGTGA	300		
Db	241	ACGGCTGTTA	CTCAGCCTC	CAAGAGCT	GTGGCCACCT	TGCGCAG	ACCGAAGTGA	300		
QY	301	GCAAGTGA	GATTC	CTCCAGACG	ATCAGACTA	CTACACAGG	ACCTTCAGT	TTGAAGTGA	360	
Db	301	GCAAGTGA	GATTC	CTCCAGACG	ATCAGACTA	CTACACAGG	ACCTTCAGT	TTGAAGTGA	360	
QY	361	ACTCGGAAT	CCGAAGTT	GGGACCC	CGGGGGCC	AGAGGGCT	GCGGCTCCGCTCA	420		
Db	361	ACTCGGAAT	CCGAAGTT	GGGACCC	CGGGGGCC	AGAGGGCT	GCGGCTCCGCTCA	420		
QY	421	GCACCCCTCA	ACGGCGA	ATCAGCC	CTGATCAG	CGCCGAG	CGGCATG	CTGCGAGC	480	
Db	421	GCACCCCTCA	ACGGCGA	ATCAGCC	CTGATCAG	CGCCGAG	CGGCATG	CTGCGAGC	480	
QY	481	ATCGATCT	TGTGTG	CTGAGACG	CGCTCCC	CAGGGAC	CGGGCGG	ACCCGACCAT	540	
Db	481	ATCGATCT	TGTGTG	CTGAGACG	CGCTCCC	CAGGGAC	CGGGCGG	ACCCGACCAT	540	
QY	541	GGGCAAG	AGAAATTA	CGTCTG	TGGGTCT	CCCCC	ACCGGCTG	CGCGATCT	600	
Db	541	GGGCAAG	AGAAATTA	CGTCTG	TGGGTCT	CCCCC	ACCGGCTG	CGCGATCT	600	
QY	601	AGAAACA	ACCGATCG	GGGGC	ACATGG	CGCCCTTA	CTGCATCA	AGCCTGG	660	
Db	601	AGAAACA	ACCGATCG	GGGGC	ACATGG	CGCCCTTA	CTGCATCA	AGCCTGG	660	
QY	661	GAGGCACT	GGGAGAG	AGGGCG	CTCTCT	CTGACAC	CACTAAGT	CACACAG	720	
Db	661	GAGGCACT	GGGAGAG	AGGGCG	CTCTCT	CTGACAC	CACTAAGT	CACACAG	720	
QY	721	GGGGTGG	AGATTC	CACTCG	TGTGTTCT	ATTTTTT	GAAAA	GACACATTT	780	
Db	721	GGGGTGG	AGATTC	CACTCG	TGTGTTCT	ATTTTTT	GAAAA	GACACATTT	780	
QY	781	TCAGTTT	TGGGCTTC	CAAGTTT	CGAGAAAT	TGCTTT	GTATTA	GTATTA	840	
Db	781	TCAGTTT	TGGGCTTC	CAAGTTT	CGAGAAAT	TGCTTT	GTATTA	GTATTA	840	
QY	841	CACCGACT	GAAATAT	TGTTT	CAATTA	TTCTG	TGGGCTG	TTTTTT	900	
Db	841	CACCGACT	GAAATAT	TGTTT	CAATTA	TTCTG	TGGGCTG	TTTTTT	900	
QY	901	AATTAAT	TAAATG	TGTG	AAAAAAA	926				
Db	901	AATTAAT	TAAATG	TGTG	AAAAAAA	926				

RESULT 3	AX578013	LOCUS	AX578013	926 bp	DNA	linear	PAT 08-JAN-2003
DEFINITION	Sequence	135	from Patent WO02081745.				
ACCESSION	AX578013						
VERSION	AX578013.1	GI:27647221					



KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
AUTHORS Garcia, T., Roman Roman, S., Baron, R., Call, K., Theilhaber, J.,  
Connolly, T., Jackson, A., Bushnell, S.E. and Rawadi, G.  
TITLE Genes involved in osteogenesis, and methods of use  
JOURNAL Patent: WO 02081745-A 135 17-OCT-2002;  
Aventis Pharma S.A. (FR)  
FEATURES  
source 1..926  
location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 100.0%; Score 926; DB 6; Length 926;  
Best Local Similarity 100.0%; Pred. No. 8.8e-174;  
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGCCCATTTCTGTTTCAAGCAGTGCAGCAAGATCATGAAGTCCGACATGACACACG 60  
DB 1 GGGGCCCATTTCTGTTTCAAGCAGTGCAGCAAGATCATGAAGTCCGACATGACACACG 60  
QY 61 CCACCGCCGCGGGGCCCGCAGCTGCGGCTGAAGGCGGCAAGACAGCGAGCGGTGCGG 120  
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VERSION X77956.1 GI:457784  
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AUTHORS Nucleotide sequence of the cDNA encoding human helix-loop-helix  
TITLE Id-1 protein: identification of functionally conserved residues  
JOURNAL common to Id proteins  
MEDLINE Biochim. Biophys. Acta 1219 (1), 160-162 (1994)  
PUBMED 94368847  
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2 (bases 1 to 926)  
AUTHORS Deed, R.  
TITLE Direct Submission  
JOURNAL Submitted (25-FEB-1994) R. Deed, Paterson Institute for Cancer  
Research, Dept of Regulation, Christie Hospital NHS Trust, Wilmslow  
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REFERENCE  
AUTHORS  
1 (bases 1 to 981)  
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klauser, R.D., Collins, F.S., Wagner, L., Shemen, C.M., Schuler, G.D.,  
Altshuler, S.F., Zeeberg, B., Buecaw, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Sapich, M., Soares, M.B., Bonaldo, M.F., Casavani, T.L.,  
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Carninci, P., Prange, C., Rana, S.S., Loughlin, N.A., Peters, G.J.,  
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Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Holyk, S.W.,  
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,  
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Rodriguez, S.,  
Bouffard, G.G., Blakeley, R.C., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalka, U., Smalls, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
human and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932

JOURNAL  
PUBMED  
2 (bases 1 to 981)  
Straussberg, R.  
Direct Submission  
Submitted (15-NOV-2000) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

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Gaithersburg, Maryland,  
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Contact: [nisc.mgc@nih.gov](mailto:nisc.mgc@nih.gov)  
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## ORIGIN

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Query Match      97.8%; Score 905.2; DB 9; Length 981;
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## RESULT 6

## LOCUS

## DEFINITION

BC012420 Homo sapiens inhibitor of DNA binding 1, dominant negative helix-loop-helix protein, transcript variant 1, mRNA (CDNA clone MGC:9178 IMAGE:3862019), complete cds.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## PUBMED

## REFERENCE

## AUTHORS

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## AUTHORS

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLNT at: <http://image.llnl.gov>

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## ORIGIN

Query Match 97.8%; Score 905.2; DB 9; Length 993;  
 Best Local Similarity 99.4%; Pred. No. 1.2e-169;  
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QY 4 GCCCATTTCTGTTTCAGCCAGTCCCAAGAAATCATGAAGTCGCGAGTGCACACCCGCA 63
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## REFERENCE

1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, B.W.  
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ACCESSION AR206590  
VERSION AR206590.1 GI:21505240  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 4793)  
AUTHORS Baker,B.F., Bennett,C.Frank, and Wyate,J.  
TITLE Antisense modulation of inhibitor of DNA binding-1 expression  
JOURNAL Patent: US 6372433-A 10 16-APR-2002;  
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Best Local Similarity 78.7%; Pred. No. 1.9e-118;  
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RESULT 9

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	VERSION	U57645.1				
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	SOURCE					
	ORGANISM	Homo sapiens (human)				
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	AUTHORS	Nehlin,J.O., Hara,E., Kuo,W.-L., Collins,C. and Campisi,J.				
	TITLE	Genomic organization, sequence and chromosomal localization of the human helix-loop-helix Id1 gene				
	JOURNLT	Biochem. Biophys. Res. Commun. (1997) In press				
	REFFERENCE	2 (bases 1 to 4793)				
	AUTHORS	Nehlin,J.O., Hara,E. and Campisi,J.				
	TITLE	Direct Submission				
	JOURNAL	Submitted (06-MAY-1996) Jan O. Nehlin, Cancer Biology, Lawrence Berkeley National Laboratory, University of California, Berkeley Rd., Bldg. 70A-1118, Berkeley, CA 94720, USA				
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LOCUS Homo sapiens chromosome 20 clone RP11-778F12 map 20, WORKING DRAFT  
DEFINITION SEQUENCE, 35 unordered pieces.  
AC023459  
AC023459.2 GI:7212060  
VERSION HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE 1 (bases 1 to 146574)  
Birken, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,  
Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavsky, L.,  
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Wu, X., Wymann, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and  
Zody, M.  
Direct Submission  
Submitted (14-FEB-2000) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 9, 2000 this sequence version replaced GI:6970679.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence.submissions@genome.wi.mit.edu  
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Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.960731  
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Quality coverage: 3.3 in Q20 bases; sum-of-contacts

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\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 35 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
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Query Match 70.0%; Score 648; DB 2; Length 146574;  
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AUTHORS Oda,K., Nakada,S., Hara,E., Yamaguchi,T., Nakamura,T., Oka,Y. and Kishimoto,T.  
TITLE HUMAN ID GENE  
JOURNAL Patent: JP 1994141864-A 1 24-MAY-1994;  
SOMITOMO ELECTRIC IND LTD  
OS Homo sapiens (human)  
PN JP 1994141864-A/1  
PD 24-MAY-1994  
PF 13-NOV-1992 JP 1992328391  
PI ODA KOICHIROU, NAKADA SUSUMU, HARA EIJI, YAMAGUCHI TOMOKO, PI  
NAKAMURA TAKESHI, OKA YUMIKO, KISHIMOTO TOSHIHIKO PC  
C12N15/12, C07H21/04, C07K13/00, C12N1/21, C12Q1/68//A61K31/70, PC  
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QY 75 GGGCCAGCTGCGCGCTGAAAGCCGCGCAAGACAGCGAGCGGTGCGGAGGTGGTGGC 134  
DB 61 GGGCCAGCTGCGCGCTGAAAGCCGCGCAAGACAGCGAGCGGTGCGGAGGTGGTGGC 120  
QY 135 TGTCTGTGAGCAAGAGCGTGCATCTTCGCGCTGCCGGGCGCCGCGCTGCT 194  
DB 121 TGTCTGTGAGCAAGAGCGTGCATCTTCGCGCTGCCGGGCGCCGCGCTGCT 180  
QY 195 GGCCTGTGAGAGAGAGAGTAAAGTGCCTCTACGACATGAACGGCTGTTACTCA 254  
DB 181 GGCCTGTGAGAGAGAGAGTAAAGTGCCTCTACGACATGAACGGCTGTTACTCA 240  
QY 255 GGCCTCAAGAGAGCTGTGCCCACTCTGCCCGCAAGACCGCAAGTGAAGAGTGAATT 314  
DB 241 GGCCTCAAGAGAGCTGTGCCCACTCTGCCCGCAAGACCGCAAGTGAAGAGTGAATT 300  
QY 315 CTCGACAGCTGATGACTATCATCAGGAGACCTTTCAGTTGAGTGAACCTCGAAATCCGAA 374  
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QY 375 GTTGGAGACCCCGGGGGCGAGAGGCTGCGGCTCGGGGCTCGCTCAGAACCTCAAGCGC 434  
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QY 435 GAGATCAGCGCCCTGTAAGCGCGCGAGCGGATGCGTTCTCTGCGAGCATGCGATCTTGTGT 494  
DB 421 GAGATCAGCGCCCTGTAAGCGCGCGAGCGGATGCGTTCTCTGCGAGCATGCGATCTTGTGT 480  
QY 495 GCGTGAAGCGCTCCCCAGAGGACCGGCGG 524  
DB 481 GCGTGAAG-GCGTTCCTCCAGAGGACCGGCGG 509  
RESULT 13

HUMID1HA 509 bp mRNA linear PRI 14-FEB-2003  
LOCUS HUMID1HA  
DEFINITION Homo sapiens mRNA for Id-1H, complete cds.  
ACCESSION D13889  
VERSION D13889.1 GI:464181  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Hara,E., Yamaguchi,T., Nojima,H., Ide,T., Campisi,J., Okayama,H.  
and Oda,K.  
TITLE Id-related genes encoding helix-loop-helix proteins are required  
for G1 progression and are repressed in senescent human fibroblasts  
J. Biol. Chem. 269 (3), 2139-2145 (1994)  
MEDLINE 94124570  
PUBMED 8294468  
REFERENCE  
AUTHORS Hara,E.  
TITLE Direct Submission  
JOURNAL Submitted (07-DEC-1992) Eiji Hara, Science University of Tokyo,  
Dept. of Biol. Science & Technol.; 2641 Yamazaki, Noda, Chiba 278,  
Japan (Tel:81-471-24-1501 (ex.4421), Fax:81-471-25-1841)  
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ORIGIN  
Query Match 52.9%; Score 490; DB 9; Length 509;  
Best Local Similarity 98.8%; Pred. No. 3.8e-87;  
Matches 504; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
QY 15 TTCAGCAATCGCCCAAGATCATGAAAGTCGCCAGTGGCAGACCCGCCCGCCG 74  
DB 1 TTCAGCAATCGCCCAAGATCATGAAAGTCGCCAGTGGCAGACCCGCCCGCCG 60  
QY 75 GGGCCAGCTGCGCGCTGAAAGCCGCGCAAGACAGCGAGCGGTGCGGAGGTGGTGGC 134  
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QY 135 TGTCTGTGAGCAAGAGCGTGCATCTTCGCGCTGCCGGGCGCCGCGCTGCT 194  
DB 121 TGTCTGTGAGCAAGAGCGTGCATCTTCGCGCTGCCGGGCGCCGCGCTGCT 180  
QY 195 GGCCTGTGAGAGAGAGAGTAAAGTGCCTCTACGACATGAACGGCTGTTACTCA 254  
DB 181 GGCCTGTGAGAGAGAGAGTAAAGTGCCTCTACGACATGAACGGCTGTTACTCA 240  
QY 255 GGCCTCAAGAGAGCTGTGCCCACTCTGCCCGCAAGACCGCAAGTGAAGAGTGAATT 314  
DB 241 GGCCTCAAGAGAGCTGTGCCCACTCTGCCCGCAAGACCGCAAGTGAAGAGTGAATT 300  
QY 315 CTCGACAGCTGATGACTATCATCAGGAGACCTTTCAGTTGAGTGAACCTCGAAATCCGAA 374

Db 301 CTCGACGACGTCATCGATCATCATGAGGAGCCTTTCAGTTGAGTGAAGTCCGAATCCGAA 360  
QY 375 GTTGGAGACCCCGGGGGGCGGAGGGGCTGCGGAGTCCGGGGCTCGCTCAGACACCTCAACGGC 434  
Db 361 GTTGAACCCCGGGGGGCGGAGGGCTGCGGAGTCCGGGGCTCGCTCAGACACCTCAACGGC 420  
QY 435 GAGATCAGGCGCCTGACGCGCCGAGGCGGAGTCCGTTCTCGCGAGATCGATCTTGTGT 494  
Db 421 GAGATCAGGCGCCTGACGCGCCGAGGCGGAGTCCGTTCTCGCGAGATCGATCTTGTGT 480  
QY 495 CGCTGAAGCGCTCCCGGAGGAGCGGCGG 524  
Db 481 CGCTGAAG-GCCTTCCCGAGGAGCGGCGG 509

RESULT 14  
LOCUS 122507 509 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 1 from patent US 5527897.  
ACCESSION 122507  
VERSION 122507.1 GI:1602861  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 (bases 1 to 509)  
Oda,K., Nakada,S., Hara,E., Yamaguchi,T., Nakamura,T., Oka,Y. and  
Kishimoto,T.  
TITLE Human ID genes  
JOURNAL Patent: US 5527897-A 1 18-JUN-1996;  
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source 1..509  
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Query Match 52.7%; Score 488.4; DB 6; Length 509;  
Best Local Similarity 98.6%; Pred. No. 7,8e-87;  
Matches 503; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 15 TTCAGCCAGTGCACCAAGATCATGAAAGTGCAGTGGAGACCGCCACCGCGCGG 74  
Db 1 TTCAGCCAGTGCACCAAGATCATGAAAGTGCAGTGGAGACCGCCACCGCGCGG 60  
QY 75 GGGCCCCAGTGGCGCTGAAAGCCCGGCAAGACAGAGCGGTGGCGGAGGTGTGCGC 134  
Db 61 GGGCCCCAGTGGCGCTGAAAGCCCGGCAAGACAGAGCGGTGGCGGAGGTGTGCGC 120  
QY 135 TGTCTGTGACAGAGCGTGGCATCTGCGGCTGCGGGGGCGGGGGCGGCGTGCCT 194  
Db 121 TGTCTGTGACAGAGCGTGGCATCTGCGGCTGCGGGGGCGGGGGCGGCGTGCCT 180  
QY 195 GCGCTGCTGACAGAGCGAGGTAAACGTGCTGCTCAAGCATGAAACGGCTGTTACTCA 254  
Db 181 GCGCTGCTGACAGAGCGAGGTAAACGTGCTGCTCAAGCATGAAACGGCTGTTACTCA 240  
QY 255 GCGCTCAAGAGAGTGGTCCCAACCTGCGGCAAGACCGAGGTGACAGAGGTGAATT 314  
Db 241 GCGCTCAAGAGAGTGGTCCCAACCTGCGGCAAGACCGAGGTGACAGAGGTGAATT 300  
QY 315 CTCGACGACGTGATGATCATCATGAGGAGCCTTCAAGTTGAGAGTCAAGTCCGAA 374  
Db 301 CTCGACGACGTGATGATCATCATGAGGAGCCTTCAAGTTGAGAGTCAAGTCCGAA 360  
QY 375 GTTGGAGACCCCGGGGGGCGGAGGGCTGCGGAGTCCGGGGCTCGCTCAGACACCTCAACGGC 434  
Db 361 GTTGAACCCCGGGGGGCGGAGGGCTGCGGAGTCCGGGGCTCGCTCAGACACCTCAACGGC 420  
QY 435 GAGATCAGGCGCCTGACGCGCCGAGGCGGAGTCCGTTCTCGCGAGATCGATCTTGTGT 494  
Db 421 GAGATCAGGCGCCTGACGCGCCGAGGCGGAGTCCGTTCTCGCGAGATCGATCTTGTGT 480  
QY 495 CGCTGAAGCGCTCCCGGAGGAGCGGCGG 524

Db 481 CGCTGAAG-GCCTTCCCGAGGAGCGGCGG 509

RESULT 15  
LOCUS AX017857 578 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 36 from Patent WO9946375.  
ACCESSION AX017857  
VERSION AX017857.1 GI:10042460  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1  
Schmitz,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and  
Pilarczyk,C.  
TITLE Human nucleic acid sequences from prostate tissue  
JOURNAL Patent: WO 9946375-A 36 16-SEP-1999;  
SCHMITZ ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN  
BERND (DE); ROSENTHAL ANDRE (DE); METAGEN GBS FUER GENOMFORSCHUN  
(DE); PILARSKY CHRISTIAN (DE)  
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ORIGIN  
Query Match 52.7%; Score 487.8; DB 6; Length 578;  
Best Local Similarity 98.8%; Pred. No. 1e-86;  
Matches 513; Conservative 0; Mismatches 2; Indels 4; Gaps 2;

QY 4 GCCATTCTGTTTACGACGAGTCGCCAAGATCATGAAAGTGCAGTGGAGACCGGCCA 63  
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QY 64 CCGCGCGCGCGGCGCCGAGCTGCGGCTGGAAGCCGGGCAAGACCGAGCGGTGGGGCG 123  
Db 121 CCGCGCGCGCGGCGCCGAGCTGCGGCTGGAAGCCGGGCAAGACCGAGCGGTGGGGCG 180  
QY 124 AGGTGCGCGCTGCTGCTGAGCAGAGCGTGGCATCTCGGCTG---CCGGGCGCGG 180  
Db 181 AGGTGCGCGCTGCTGCTGAGCAGAGCGTGGCATCTCGGCTGCGCGGGGCGCGG 240  
QY 181 GGGCGCGCGCTGCTGCTGAGCAGAGCGTGGCATCTCGGCTGCGCGGGGCGCGG 240  
Db 241 GGGCGCGCGCTGCTGCTGAGCAGAGCGTGGCATCTCGGCTGCGCGGGGCGCGG 300  
QY 241 ACGGCTGTTACTCAGCGCTCAAGAGCTGTGCCCAACCTGCCCAAGAACCGCAAGTGA 300  
Db 301 ACGGCTGTTACTCAGCGCTCAAGAGCTGTGCCCAACCTGCCCAAGAACCGCAAGTGA 360  
QY 301 GCAAGGTGGAATTCACAGACGTCATCGATCATGAGGAGCCTTCAAGTTGAGCTGA 360  
Db 361 GCAAGGTGGAATTCACAGACGTCATCGATCATGAGGAGCCTTCAAGTTGAGCTGA 420  
QY 361 ACTCGGAATTCGAAGTTGAGACCCCGGGGGGCGGAGGCTGCGGCTCGGCTCA 420  
Db 421 ACTCGGAATTCGAAGTTGAGACCCCGGGGGGCGGAGGCTGCGGCTCGGCTCA 480  
QY 421 GCAACCTCAAGCGGAGATCAAGCGGCTGACGCGCCGAGGCGGAGTCTTCTCGGAGC 480  
Db 481 GCAACCTCAAGCGGAGATCAAGCGGCTGACGCGCCGAGGCGGAGTCTTCTCGGAGC 540  
QY 481 ATCGCATCTTGTGCTGAGAGCGGCTCCCGGAGGAGC 519  
Db 541 ATCGCATCTTGTGCTGAGAG-GCCTCCCGGAGGAGC 578

Search completed: December 18, 2004, 18:12:40  
Job time : 4154.34 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2004, 13:49:15 ; Search time 508.452 Seconds  
(without alignment)  
9560.323 Million cell updates/sec

Title: US-09-996-529A-4

Perfect score: 926  
Sequence: 1 gggggcccttcgttcagc.....ttgatggtgaaaaaaaaa 926

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	926	100.0	926	6	AA616579 DNA encod
2	926	100.0	926	6	AB234777 Coding se
3	926	100.0	926	10	ADG89363 Cancer de
4	926	100.0	926	12	ADJ75169 Marker ge
5	926	100.0	926	12	ADN04358 Antipsoi
6	905.2	97.8	993	12	AD124460 Human mod
7	897.2	96.9	979	5	AA644963 CDNA enco
8	893.2	96.5	1027	3	AA18245 Lung canc
9	648	70.0	4793	6	AA16586 DNA encod
10	622	67.2	1216	2	AA233520 Human pro
11	510.6	55.1	682	10	AB283034 Tox1colog
12	490	52.9	509	2	AAQ66082 Human id-
13	466	50.3	481	6	ABV78155 Human ID1
14	466	50.3	481	6	AB235731 Human ID1
15	466	50.3	481	6	ABX09974 Human ID1
16	466	50.3	481	6	ABX16596 Human pol
17	447.8	48.4	483	8	AB234702 Coding se
18	443.6	47.9	958	12	ADJ77697 Human inh
19	442.2	47.8	721	2	AA440105 Gastric c
20	439.2	47.4	502	2	AAQ66083 Human id-
21	424.8	45.9	927	6	AB199635 Mouse 1ec

22	424.8	45.9	927	12	ADJ76041 Marker ge
23	371.8	40.2	434	10	ADK12090 Breast ca
24	343.4	37.1	1049	5	AA645151 CDNA enco
25	341.6	36.9	461	2	AA440106 Gastric c
26	289	31.2	1124	6	ABK63667 Rat seque
27	289	31.2	1124	10	ADB58118 Toxicity-
28	289	31.2	1124	10	ADB52602 Primary r
29	289	31.2	1124	12	ADP72604 Renal tox
30	283	30.6	431	3	AA69712 Human bre
31	271.4	29.3	630	6	ABT09474 Phase-1 R
32	271.4	29.3	630	10	ADG30912 Liver tox
33	271.4	29.3	630	12	ADG45499 Liver inf
34	271.4	29.3	630	12	ADH22801 Partial D
35	269	29.0	1553	6	ABQ67145 Human ang
36	268.2	29.0	1553	6	ABQ67146 Human ang
37	255.4	27.6	319	3	AA698395 Human col
38	219.4	23.7	256	6	ABK53839 Human hea
39	216.8	23.4	265	6	ABK53822 Human hea
40	210.4	22.7	217	6	ABK53894 Human hea
41	207.2	22.4	224	6	ABK53985 Human hea
42	207.2	22.4	224	6	ABK53986 Human hea
43	205.4	22.2	213	6	ABK53845 Human hea
44	199.4	21.5	201	6	ABK53900 Human hea
45	197	21.3	378	8	ABx48664 Bovine ES

## ALIGNMENTS

RESULT 1	AA616579	standard; CDNA, 926 BP.
ID	AA616579	
AC	AA616579	
XX		
DT	14-FEB-2002	(first entry)
XX		
DE	DNA encoding human inhibitor of DNA binding-1.	
XX		
KW	Human; inhibitor of DNA binding-1; Id-1; cytostatic; antiinflammatory;	
KW	immunosuppressive; antisense therapy; antisense oligonucleotide;	
KW	hyperproliferative disorder; immune disorder; muscular disorder; ss;	
KW	vascular disorder; pancreatic disorder; infection; inflammation; tumour.	
OS	Homio sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	36..500
FT		/*tag= a
FT		/product= "Inhibitor of DNA binding-1"
PN	WO200183513-A2.	
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PD	08-NOV-2001.	
XX		
PF	25-APR-2001; 2001WO-US013209.	
XX		
PR	28-APR-2000; 2000US-00561497.	
XX		
PA	(ISIS-) ISIS PHARM INC.	
XX		
PI	Baker BF, Bennett CF, Wyatt JR;	
XX		
DR	WPI; 2002-041477/05.	
XX		
DR	P-PSDB; AAU10351.	
XX		
PT	Novel antisense compound, specifically hybridizing to and inhibiting the	
PT	expression of Inhibitor of DNA binding-1, useful for treating disorder.	
PT	hyperproliferative, immune, muscular, vascular or pancreatic disorder.	
XX		
PS	Example 13; Page 87-88; 105pp; English.	
XX		
CC	The invention relates to novel antisense compounds (I) 8-30 nucleobases	

in length targeted to a nucleic acid molecule encoding inhibitor of DNA binding-1, where (I) specifically hybridises with and inhibits the expression of inhibitor of DNA binding-1. Antisense inhibition of human inhibitor of DNA binding-1 expression by chemical phosphorochlorate oligonucleotides having 2'-methoxyethyl (2'-MOE) wings and a deoxy gap was tested. A series of oligonucleotides were designed to target different regions of the human inhibitor of DNA binding-1 RNA. The compounds were analysed for their effect on human inhibitor of DNA binding-1 mRNA levels by quantitative real-time polymerase chain reaction (PCR). The result showed that the oligonucleotides showed at least 25% inhibition of human inhibitor of DNA binding-1 expression. (I) is useful for inhibiting the expression of inhibitor of DNA binding-1 in cells or tissues by contacting the cells or tissues with (I). (I) is also useful for treating a human having a disease or condition associated with inhibitor of DNA binding-1 by administering a therapeutically or prophylactically effective amount of (I), where the disease or condition is a hyperproliferative disorder, immune disorder, muscular disorder, vascular disorder or pancreatic disorder. (I) may also be used for diagnostics, therapeutics, prophylaxis (e.g., to prevent or delay infection, inflammation or tumour formation), and as research reagents and kits. (I) may be safely and effectively administered to humans. The present sequence represents the coding sequence of human inhibitor of DNA binding-1, which was used to design the antisense oligonucleotides of the invention.

sequence 926 BP; 193 A; 262 C; 281 G; 190 T; 0 U; 0 Other;

Query Match	100.0%;	Score 926;	DB 6;	Length 926;
Best Local Similarity	100.0%;	Pred. No. 1.5e-219;		
Matches 926;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	1	GGGGGCCCAATCTGTGTTTCAAGCCAGTGGCCCAAGATCATGAAATGTGCGAGTGGCAGACCG	60
Db	1	GGGGGCCCAATCTGTGTTTCAAGCCAGTGGCCCAAGATCATGAAATGTGCGCGAGTGGCAGACCG	60
QY	61	CCACCGCGCGCGCGGAGCCCGCAGCTCGCGCTAAAGCGCGGCAAGACAGAGCGGTGGCG	120
Db	61	CCACCGCGCGCGCGGAGCCCGCAGCTCGCGCTAAAGCCCGCAGACAGAGCGGTGGCG	120
QY	121	GCGAGTGTGTGGCGCTGTCTGTCTAGAGAGAGGTGGCCATCTCGCGCTGCGGAGCGCG	180
Db	121	GCGAGTGTGTGGCGCTGTCTGTCTAGAGAGAGGTGGCCATCTCGCGCTGCGGAGCGCG	180
QY	181	GCGCGCGCTGTGCTGTGCTGTGACGAGCAGCAGAGTAAAGTGTGTCTTACGACATGA	240
Db	181	GCGCGCGCTGTGCTGTGCTGTGACGAGCAGCAGAGTAAAGTGTGTCTTACGACATGA	240
QY	241	ACGCGTGTATCTACGCGCTCAAGAGAGGTGTGGCCACCTTCGCCCAAGACCGCAAGTGA	300
Db	241	ACGCGTGTATCTACGCGCTCAAGAGAGGTGTGGCCACCTTCGCCCAAGACCGCAAGTGA	300
QY	301	GCAAGGTGTGAGATTCTCCAGCAGTTCATCGACTCATCAGGAGCCTTCAGTTGAGCTGA	360
Db	301	GCAAGGTGTGAGATTCTCCAGCAGTTCATCGACTCATCAGGAGCCTTCAGTTGAGCTGA	360
QY	361	ACTCGGAATCCGAAGTTGGAGACCCCGGAGGCGCGAGGGCTTCGCGTCCGCGTCA	420
Db	361	ACTCGGAATCCGAAGTTGGAGACCCCGGAGGCGCGAGGGCTTCGCGTCCGCGTCA	420
QY	421	GCACCTTCGAACGCGGAGATCAGCGCCCTGACGCGCAGCGAGCGATGCGTTCCTGCGGACG	480
Db	421	GCACCTTCGAACGCGGAGATCAGCGCCCTGACGCGCAGCGAGCGATGCGTTCCTGCGGACG	480
QY	481	ATGCAATCTTGTGTGCGCTGAAGGCGCTCCCGCAGGAGCGGCGGATCCCAAGCATTCAGG	540
Db	481	ATGCAATCTTGTGTGCGCTGAAGGCGCTCCCGCAGGAGCGGCGGATCCCAAGCATTCAGG	540
QY	541	GGGCAGAAGAAATTACGTGCTGTGGGTCTCCCGCAGCGGCTGCGCGGATCTAGGG	600
Db	541	GGGCAGAAGAAATTACGTGCTGTGGGTCTCCCGCAGCGGCTGCGCGGATCTAGGG	600
QY	601	AGAAACAAGACGATTCGGCGGCGCATGCGCCCTTAATTCGATCCAGCTGGGCTGAGGCT	660
Db	601	AGAAACAAGACGATTCGGCGGCGCATGCGCCCTTAATTCGATCCAGCTGGGCTGAGGCT	660

Db	601	AGAAACAAGCCGATCGGCGGCGCACCTGGCCCTTAATCTGCATCCAGCCTGGGGCTGAAGCT	666
Qy	661	GAGGCACTGGCGCAGAGAGAGGGCGCTCTCTCTGCACACTAATAGTCACAGAGACTTTA	720
Db	661	GAGGCACTGGCGCAGAGAGGGCGCTCTCTCTGCACACTAATAGTCACAGAGACTTTA	720
Qy	721	GGGGGTGGGATTCACCTCGTGTGTTCTAATTTTGAAGAGACATTTTAAAGAAATGG	780
Db	721	GGGGGTGGGATTCACCTCGTGTGTTCTAATTTTGAAGAGACATTTTAAAGAAATGG	780
Qy	781	TCACGTTTGGGTCCTCTCAGATTTCTGAGGAAATTCGTTTGTAATGTATATTAACAATGAT	840
Db	781	TCACGTTTGGGTCCTCTCAGATTTCTGAGGAAATTCGTTTGTAATGTATATTAACAATGAT	840
Qy	841	CACCGACTGAGAAATATGTTTACAAATAGTCTGTGGGCGCTGTTTTTTTGTATTAACA	900
Db	841	CACCGACTGAGAAATATGTTTACAAATAGTCTGTGGGCGCTGTTTTTTTGTATTAACA	900
Qy	901	AATATTTAGATGGTGAAGAAAAAAA 926	
Db	901	AATATTTAGATGGTGAAGAAAAAAA 926	

## RESULT 2

ABZ34777 standard; cDNA; 926 BP.

AC ABZ34777;

04-FEB-2003 (first entry,  
XX

XX counting sequence SEQ ID 135, upregulated in osteogenesis

KM osteopetrosis; bone disease; downregulator; human; transcription factor orphan nuclear receptor; ss.

US      Homo sapiens  
XX

[illegible]

XX

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useful for bone disease therapy in subject.

claim 26; page 150-151; 237pp; English.

present, invention relates to novel nucleotide sequences, which are differentially expressed in models of osteogenesis upon being put in contact with a stimulator of osteogenesis. The present sequence is one such sequence. This sequence can be used for diagnosing osteoporosis/bone disease in a patient, promoting osteogenesis and/or preventing osteoporosis/bone disease. The present sequence encodes a transcription factor or an orphan nuclear receptor.

sequence 320 BF; 193 A; 262 C; 281 G; 190 T; 0 U; 0 Other;

Query Match	100.0%;	Score 926;	DB 8;	Length 926;
Best Local Similarity	100.0%;	Pred. No. 1.5e-219;		
Matches 926;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

```
QY 1 GGGGCCCATCTGTTTCAAGCAGTGCAGAAATCATGAAAGTCGCGACGAGACACG 60
DB 1 GGGGCCCATCTGTTTCAAGCAGTGCAGAAATCATGAAAGTCGCGACGAGACACG 60
QY 61 CCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
DB 61 CCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
QY 121 GCGAGTGTGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 180
DB 121 GCGAGTGTGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 180
QY 181 GGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 181 GGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 ACGGCTGTCTCAAGCCTCAAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 241 ACGGCTGTCTCAAGCCTCAAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 GCAAGTGTGAATTTCTCAAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 301 GCAAGTGTGAATTTCTCAAGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 ACTGGGAATCCGAAGTGTGGAACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCT 420
DB 361 ACTGGGAATCCGAAGTGTGGAACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCT 420
QY 421 GCACCTTCAAGCGCGAGATTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 421 GCACCTTCAAGCGCGAGATTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 481 ATTCGATCTTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 ATTCGATCTTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 GGGGCAAGGAATTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
DB 541 GGGGCAAGGAATTAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
QY 601 AGAACAAGACGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 660
DB 601 AGAACAAGACGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 660
QY 661 GAGGCACTGTGCGAGAGAGGCGCTCTCTCTGCAACCTACTAGTCAACAGACTT 720
DB 661 GAGGCACTGTGCGAGAGAGGCGCTCTCTCTGCAACCTACTAGTCAACAGACTT 720
QY 721 GGGGCTGGGATTCACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
DB 721 GGGGCTGGGATTCACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
QY 781 TCACGTTTGTGCTCTCAGATTTCTGAGGAATGCTTTGATTTGATTTATTAATAT 840
DB 781 TCACGTTTGTGCTCTCAGATTTCTGAGGAATGCTTTGATTTGATTTATTAATAT 840
QY 841 CACCGACTGAGAAATTTGTTTACAAATAGTCTGTGTGTGTGTGTGTGTGTGTGT 900
DB 841 CACCGACTGAGAAATTTGTTTACAAATAGTCTGTGTGTGTGTGTGTGTGTGTGT 900
QY 901 AATAATTTAGATGTGAAAAAAA 926
DB 901 AATAATTTAGATGTGAAAAAAA 926
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RESULT 3  
ADG89363 standard; DNA; 926 BP.  
XX  
AC ADG89363;  
XX  
DT 11-MAR-2004 (first entry)  
XX

```
DE Cancer detection method related gene #26.  
XX ds; cancer; gene expression;  
KM estrogen receptor-positive invasive breast cancer.  
OS Homo sapiens.  
XX MO2003078662-A1.  
XX 25-SEP-2003.  
XX 12-MAR-2003; 2003WO-US007713.  
XX 13-MAR-2002; 2002US-0364890P.  
XX 18-SEP-2002; 2002US-0412049P.  
XX (GENO-) GENOMIC HEALTH INC.  
PA Baker JB, Cronin MT, Kiefer MC, Shak S, Walker MG;  
PI WPI; 2003-767536/72.  
XX  
XX Predicting clinical outcome for a patient diagnosed with cancer comprises  
PT determining the expression level of one or more genes, and compared to  
PT the amount found in a reference cancer tissue set.  
XX  
XX Disclosure; SEQ ID NO 311, 198pp; English.  
XX  
XX The invention relates to a method of predicting clinical outcome for a  
CC patient diagnosed with cancer by determining the expression level of one  
CC or more genes, or their expression products, selected from p53BP2,  
CC cathepsin B, cathepsin L, Ki67/MIB1, and thymidine kinase in a cancer  
CC tissue obtained from the patient, normalized against control gene(s), and  
CC compared to the amount found in a reference cancer tissue set. The  
CC specification also discloses an array comprising polynucleotides  
CC hybridizing to the following genes: FOXM1, PRAME, Bcl2, STK15, CEBP1, Ki-  
CC 67, GSTM1, C9, PR, BRC3, NME1, SURV, GAT3, TFR3, YB-1, DPYD, GSTJ3,  
CC RPEKB1, Sro, Chk1, ID1, Bcl2, CCR1, XIP, Chk2, CDC25B, IGF1R,  
CC AKO55699, P13K2A, TGFBR3, BAG1, CYP3A4, EPCAM, VEGFC, p52, HENT1, MIB1,  
CC HNP3A, NFKB1, BRCA2, EGFR, TKI, VDR, Contig51037, BENT1, BPHX1, IFI1,  
CC CDH1, HIF1, IGFBP3, CTSB, Her2 and DIABLO, immobilized on a solid  
CC surface. The methods are useful for predicting clinical outcome for a  
CC patient diagnosed with cancer, classifying cancer, and predicting the  
CC likelihood of long-term survival of a breast cancer patient, or a patient  
CC diagnosed with invasive breast cancer or with estrogen receptor (ER)-  
CC positive invasive breast cancer. This sequence corresponds to a gene  
CC sequence whose expression is detected by the method of the invention.  
XX  
SQ Sequence 926 BP; 193 A; 262 C; 281 G; 190 T; 0 U; 0 Other;  
Query Match 100.0%; Score 926; DB 10; Length 926;  
Best Local Similarity 100.0%; Pred. No. 1.5e-219;  
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGCCCATCTGTTTCAAGCAGTGCAGAAATCATGAAAGTCGCGACGAGACACG 60  
DB 1 GGGGCCCATCTGTTTCAAGCAGTGCAGAAATCATGAAAGTCGCGACGAGACACG 60  
QY 61 CCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120  
DB 61 CCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120  
QY 121 GCGAGTGTGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 180  
DB 121 GCGAGTGTGTGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 180  
QY 181 GGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
DB 181 GGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
QY 241 ACGGCTGTCTCAAGCCTCAAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
DB 241 ACGGCTGTCTCAAGCCTCAAGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
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QY 301 GCAAGTGAAGTATTCAGACGATCATGACATGAGGAGACCTTCAGTTGAGCTGA 360  
DB 301 GCAAGTGAAGTATTCAGACGATCATGACATGAGGAGACCTTCAGTTGAGCTGA 360  
QY 361 ACTCGAATCCGAAATTGAGACCCCGGGGGCCGAGGAGCTGCCGATCCGCTCA 420  
DB 361 ACTCGAATCCGAAATTGAGACCCCGGGGGCCGAGGAGCTGCCGATCCGCTCA 420  
QY 421 GCACCTTAAGGGGAGATTCAGCGCCCTGACGCGCCGAGGCGGATGCTTCTGCGAGC 480  
DB 421 GCACCTTAAGGGGAGATTCAGCGCCCTGACGCGCCGAGGCGGATGCTTCTGCGAGC 480  
QY 481 ATTCGATCTTGTGCTGAGAGCGCCCTCCCGAGGAGACCGGCGGACCCAGCATCCAGG 540  
DB 481 ATTCGATCTTGTGCTGAGAGCGCCCTCCCGAGGAGACCGGCGGACCCAGCATCCAGG 540  
QY 541 GGGGCAAGAGAAATTCGTGCTCTGTGGTCTTCCCGAAGCGGCTCGCGGATCTGAGGG 600  
DB 541 GGGGCAAGAGAAATTCGTGCTCTGTGGTCTTCCCGAAGCGGCTCGCGGATCTGAGGG 600  
QY 601 AGAACAAGACCGATTCGGGGGCACTGCGCCCTTAACTGCACTCAGCTGAGGCT 660  
DB 601 AGAACAAGACCGATTCGGGGGCACTGCGCCCTTAACTGCACTCAGCTGAGGCT 660  
QY 661 GAGGCACTGCGAGGAGAGGCGCTCTCTGACACCTTACTAGTACAGAGACTTTA 720  
DB 661 GAGGCACTGCGAGGAGAGGCGCTCTCTGACACCTTACTAGTACAGAGACTTTA 720  
QY 721 GGGGGTGGGATTCACCTGCTGTGTTTCTAATTTTGAAGACAGCATTTTAAAAATGG 780  
DB 721 GGGGGTGGGATTCACCTGCTGTGTTTCTAATTTTGAAGACAGCATTTTAAAAATGG 780  
QY 781 TCAGTTTGGGCTTCTCAGATTTCTGAGAAATGCTTTGATTTATTAACAATAT 840  
DB 781 TCAGTTTGGGCTTCTCAGATTTCTGAGAAATGCTTTGATTTATTAACAATAT 840  
QY 841 CACGCACTGAGAAATTTGTTTAAACAATGTTCTGAGGAGCTTTTGTATTTAAACA 900  
DB 841 CACGCACTGAGAAATTTGTTTAAACAATGTTCTGAGGAGCTTTTGTATTTAAACA 900  
QY 901 AATAATTGATGTTGAAAAAAA 926  
DB 901 AATAATTGATGTTGAAAAAAA 926

RESULT 4  
ADJ75169  
ID ADJ75169 standard; DNA; 926 BP.  
XX  
AC ADJ75169;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Marker gene SEQ ID NO:421.  
XX  
KW bronchial asthma; chronic obstructive pulmonary disease;  
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
KW gene therapy; marker gene; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN EPI394274-A2.  
PD 03-MAR-2004.  
XX  
PF 04-AUG-2003; 2003EP-00254857.  
XX  
PR 06-AUG-2002; 2002JP-00229312.  
XX  
PR 20-MAR-2003; 2003JP-00077212.  
XX  
PA (GENO-) GENOX RES INC.  
XX

PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuwara K;  
XX  
DR WPI; 2004-193155/19.  
XX  
PT Testing for bronchial asthma or chronic obstructive pulmonary disease by  
PT comparing the expression level of a marker gene in a biological sample  
PT from a subject with the expression level of the gene in a sample from a  
PT healthy subject.  
XX  
XX  
XX Claim 1; SEQ ID NO 421; 241bp; English.  
XX  
XX The present invention describes a method of testing for bronchial asthma  
XX or chronic obstructive pulmonary disease. The method comprises  
XX determining the expression level of a marker gene in a biological sample  
XX from a subject, comparing the expression level determined with the  
XX expression level of the marker gene in a biological sample from a healthy  
XX subject, and judging whether the subject has bronchial asthma or chronic  
XX obstructive pulmonary disease. The marker gene comprises: (a) a group of  
XX genes (S1) whose expression levels increase when respiratory epithelial  
XX cells are stimulated with interleukin-13; or (b) a group of genes (S2)  
XX whose expression levels decrease when respiratory epithelial cells are  
XX stimulated with interleukin-13. Also described: (1) a reagent (I) for  
XX testing for bronchial asthma or chronic obstructive pulmonary disease;  
XX (2) a kit for screening for a candidate compound for a therapeutic agent  
XX to treat bronchial asthma or chronic obstructive pulmonary disease; (3)  
XX an animal model for bronchial asthma or chronic obstructive pulmonary  
XX disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a  
XX method for producing an animal model for bronchial asthma or chronic  
XX obstructive pulmonary disease; (6) a therapeutic agent for bronchial  
XX asthma or chronic obstructive pulmonary disease, comprising the compound,  
XX a marker gene or an antisense nucleic acid corresponding to a portion of  
XX the marker gene, a ribozyme, a polynucleotide that suppresses the  
XX expression of the gene through an RNAi effect or an antibody recognising  
XX a protein encoded by a marker gene; and (7) a DNA chip for testing for  
XX bronchial asthma or a chronic obstructive pulmonary disease, on which a  
XX probe has been immobilised to assay a marker gene. (I) has respiratory  
XX and antiasthmatic activities, and can be used in gene therapy. The method  
XX is useful for testing for or screening for a therapeutic agent for  
XX bronchial asthma or chronic obstructive pulmonary disease. The present  
XX sequence is used in the exemplification of the present invention.  
SQ  
Sequence 926 BP; 193 A; 262 C; 281 G; 190 T; 0 U; 0 Other;  
Query Match 100.0%; Score 926; DB 12; Length 926;  
Best Local Similarity 100.0%; Pred. No. 1.5e-219;  
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGCCCATTCGTGTTTGAAGCCAGTCCGCAAGAAATCATGAAAGTCCAGTGGCAGCACCG 60  
DB 1 GGGGCCCATTCGTGTTTGAAGCCAGTCCGCAAGAAATCATGAAAGTCCAGTGGCAGCACCG 60  
QY 61 CCACCGCGCGCGGGGGCCCAAGCTGCGCGCTGAAAGCGCGGCAAGACGAGCGGTCCG 120  
DB 61 CCACCGCGCGCGGGGGCCCAAGCTGCGCGCTGAAAGCGCGGCAAGACGAGCGGTCCG 120  
QY 61 CCACCGCGCGCGGGGGCCCAAGCTGCGCGCTGAAAGCGCGGCAAGACGAGCGGTCCG 120  
DB 61 CCACCGCGCGCGGGGGCCCAAGCTGCGCGCTGAAAGCGCGGCAAGACGAGCGGTCCG 120  
QY 121 GCAGAGTGTGCGGTGCTGCTGAGACAGCGTGGCATCTGCGCTGCCGGGCGCCG 180  
DB 121 GCAGAGTGTGCGGTGCTGCTGAGACAGCGTGGCATCTGCGCTGCCGGGCGCCG 180  
QY 181 GGGGCGCGCTGCTGCCCTGCTGACGACGAGCAGAGGTAACGTGCTCTTACGACATGA 240  
DB 181 GGGGCGCGCTGCTGCCCTGCTGACGACGAGCAGAGGTAACGTGCTCTTACGACATGA 240  
QY 241 ACGGCTGTACTCAGACGCTCAAGAGAGTGTGCCACCTGCGCCCAAGACCGCAAGTGA 300  
DB 241 ACGGCTGTACTCAGACGCTCAAGAGAGTGTGCCACCTGCGCCCAAGACCGCAAGTGA 300  
QY 301 GCAAGTGAAGTATTCAGACGATCATGACATGAGGAGACCTTCAGTTGAGCTGA 360  
DB 301 GCAAGTGAAGTATTCAGACGATCATGACATGAGGAGACCTTCAGTTGAGCTGA 360  
QY 361 ACTCGAATCCGAAATTGAGACCCCGGGGGCCGAGGAGCTGCCGATCCGCTCA 420



Db 361 ACTCGAATCCGAAATTGGAGACCCCGGGGGCCGAGGGGCTGCGGGTCCGGCTCCGCTCA 420  
Qy 421 GCACTCTCAACGGCCAGATCAAGCCCTCTGACGGCCGAGGCGGATGCGTCTCTGGGACG 480  
Db 421 GCACCTCAACGGCCAGATCAAGCCCTCTGACGGCCGAGGCGGATGCGTCTCTGGGACG 480  
Qy 481 ATCGCATCTGTGTGCTGAAAGCGGCTCCCGAGGGAACGGGGAACCCGAGCATTCAGG 540  
Db 481 ATCGCATCTGTGTGCTGAAAGCGGCTCCCGAGGGAACGGGGAACCCGAGCATTCAGG 540  
Qy 541 GGGCAAGAGAAATTAAGTCTGTGTGTCTCTGCAACGCGCTGCGCGATTCGAGGG 600  
Db 541 GGGCAAGAGAAATTAAGTCTGTGTGTCTCTGCAACGCGCTGCGCGATTCGAGGG 600  
Qy 601 AGAACAAGACCGATGCGGGCCATGCGGCTTAACTGATCAAGCTGGGGCTGAGGCT 660  
Db 601 AGAACAAGACCGATGCGGGCCATGCGGCTTAACTGATCAAGCTGGGGCTGAGGCT 660  
Qy 661 GAGGCACTGGGAGAGAGGGGGCTCTCTGCAACGCTACTAGTCAACAGACTTAA 720  
Db 661 GAGGCACTGGGAGAGAGGGGGCTCTCTCTGCAACGCTACTAGTCAACAGACTTAA 720  
Qy 721 GGGGGTGGGAAATTCACCTGCTGTGTCTTATTTTGAAGAAGACATTTTAAAAATGG 780  
Db 721 GGGGGTGGGAAATTCACCTGCTGTGTCTTATTTTGAAGAAGACATTTTAAAAATGG 780  
Qy 781 TCACGTTTGGTCTCTCAGATTTCTGAGAAATGCTTTGATTGTATTTATCAATGAT 840  
Db 781 TCACGTTTGGTCTCTCAGATTTCTGAGAAATGCTTTGATTGTATTTATCAATGAT 840  
Qy 841 CACCGACTGAGAAATTTGTTTACAATAGTCTGTGGGGCTGTTTTTGTATTTAAACA 900  
Db 841 CACCGACTGAGAAATTTGTTTACAATAGTCTGTGGGGCTGTTTTTGTATTTAAACA 900  
Qy 901 AATAATTTAGATGTGAAAAA 926  
Db 901 AATAATTTAGATGTGAAAAA 926

RESULT 5  
ID ADN04358  
ADN04358 standard; cDNA; 926 BP.  
XX  
AC ADN04358;  
DT 01-JUL-2004 (first entry)  
DE Antipsoriatic cDNA sequence #379.  
KM ds; gene; antipsoriatic; gene therapy; psoriasis; diagnosis.  
XX  
OS Homo sapiens.  
PN WO2004028479-A2.  
PD 08-APR-2004.  
PF 25-SEP-2003; 2003WO-US030907.  
PR 25-SEP-2002; 2002US-0414006P.  
XX  
PA (GENTH ) GENEENTECH INC.  
PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WI;  
PI Wu TD;  
XX  
DR MPI: 2004-305105/28.  
DR P-PSDB; ADN04359.  
XX  
PT New PRO nucleic acid or polypeptide, useful for preparing a  
PT pharmaceutical composition for diagnosing or treating psoriasis in a  
PT mammal.  
XX

PS Claim 1; SEQ ID NO 752; 3069pp; English.  
XX  
CC The invention relates to novel polynucleotide and polypeptides for  
CC treating psoriasis or a sequence having at least 80% identity to the  
CC above sequences. The nucleic acid is useful for preparing a composition  
CC for diagnosing or treating psoriasis in a mammal. This sequence  
CC corresponds to one of the polynucleotides of the invention.  
XX  
SQ Sequence 926 BP; 193 A; 262 C; 281 G; 190 T; 0 U; 0 Other;  
Query Match 100.0%; Score 926; DB 12; Length 926;  
Best Local Similarity 100.0%; Pred. No. 1,5e-219;  
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGCCATTTCTGTTTCAAGCAGTGGCCCAAGATATGAAAGTCCGACGTGACACCG 60  
Db 1 GGGGCCATTTCTGTTTCAAGCAGTGGCCCAAGATATGAAAGTCCGACGTGACACCG 60  
Qy 61 CCACCG 120  
Db 61 CCACCG 120  
Qy 121 GCGAGTGTGCTGTCTGTCTGTAGACAGAGGTGCGCATCTCGGCTGCCGGGCGCG 180  
Db 121 GCGAGTGTGCTGTCTGTCTGTAGACAGAGGTGCGCATCTCGGCTGCCGGGCGCG 180  
Qy 181 GGGCGGCTGCTGCTGCTGCTGAGACAGACAGAGTAAAGTGTCTTACGACATGA 240  
Db 181 GGGCGGCTGCTGCTGCTGCTGAGACAGACAGAGTAAAGTGTCTTACGACATGA 240  
Qy 241 ACGGTGTATCTACAGCCTCAAGAGAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCG 300  
Db 241 ACGGTGTATCTACAGCCTCAAGAGAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCG 300  
Qy 301 GCAAGTGTGAGATTTCTCAGACAGTCACTGATCATGAGGACCTTCAGTTGAGCTGA 360  
Db 301 GCAAGTGTGAGATTTCTCAGACAGTCACTGATCATGAGGACCTTCAGTTGAGCTGA 360  
Qy 361 ACTCGGAATCCGAAAGTTGGACCCCGGGGGCCGAGGGCTGCGGCTCCGCTCA 420  
Db 361 ACTCGGAATCCGAAAGTTGGACCCCGGGGGCCGAGGGCTGCGGCTCCGCTCA 420  
Qy 421 GCACTCTCAACGGCCAGATCAAGCCCTCTGACGGCCGAGGCGGATGCGTCTGGGACG 480  
Db 421 GCACTCTCAACGGCCAGATCAAGCCCTCTGACGGCCGAGGCGGATGCGTCTGGGACG 480  
Qy 481 ATCGCATCTGTGTGCTGAAAGCGGCTCCCGAGGGAACGGGGAACCCGAGCATTCAGG 540  
Db 481 ATCGCATCTGTGTGCTGAAAGCGGCTCCCGAGGGAACGGGGAACCCGAGCATTCAGG 540  
Qy 541 GGGCAAGAGAAATTAAGTCTGTGTGTCTCTGCAACGCGCTGCGCGATTCGAGGG 600  
Db 541 GGGCAAGAGAAATTAAGTCTGTGTGTCTCTGCAACGCGCTGCGCGATTCGAGGG 600  
Qy 601 AGAACAAGACCGATGCGGGCCATGCGGCTTAACTGATCAAGCTGGGGCTGAGGCT 660  
Db 601 AGAACAAGACCGATGCGGGCCATGCGGCTTAACTGATCAAGCTGGGGCTGAGGCT 660  
Qy 661 GAGGCACTGGGAGAGAGGGGGCTCTCTGCAACGCTACTAGTCAACAGACTTAA 720  
Db 661 GAGGCACTGGGAGAGAGGGGGCTCTCTCTGCAACGCTACTAGTCAACAGACTTAA 720  
Qy 721 GGGGGTGGGAAATTCACCTGCTGTGTCTTATTTTGAAGAAGACATTTTAAAAATGG 780  
Db 721 GGGGGTGGGAAATTCACCTGCTGTGTCTTATTTTGAAGAAGACATTTTAAAAATGG 780  
Qy 781 TCACGTTTGGTCTCTCAGATTTCTGAGAAATGCTTTGATTGTATTTATCAATGAT 840  
Db 781 TCACGTTTGGTCTCTCAGATTTCTGAGAAATGCTTTGATTGTATTTATCAATGAT 840  
Qy 841 CACCGACTGAGAAATTTGTTTACAATAGTCTGTGGGGCTGTTTTTGTATTTAAACA 900  
Db 841 CACCGACTGAGAAATTTGTTTACAATAGTCTGTGGGGCTGTTTTTGTATTTAAACA 900

QY 901 AATTAATTAGATGTGAAAAAAA 926  
Db 901 AATTAATTAGATGTGAAAAAAA 926

RESULT 6  
AD124460  
ID AD124460 standard; cDNA; 993 BP.  
XX  
XX AD124460;

AC AD124460;  
DT 15-APR-2004 (first entry)  
XX

DE Human modifier of Chk1 (MCHK) encoding cDNA SEQ ID NO:10.

XX Chk1 pathway modulating agent; modifier of Chk1; MCHK; cyostatic;  
KM gene therapy; cancer; human; gene; ss.

XX Homo sapiens.

XX MO2004004785-A1.

XX 15-JAN-2004.

XX 09-JUL-2003; 2003WO-US021379.

XX 10-JUL-2002; 2002US-039484SP.

PR 16-SEP-2002; 2002US-0410986P.

XX (EXEL-) EXELIXIS INC.

XX Francis-Iang H, Roche S, Joo DM, Nicoll M, Hai B, Zhang H,

PI Lickteig K, Amundsen CD, Jin Y, Adamkewicz JI, Platt DM;

PI Hammonds RG;

XX MPI: 2004-083465/08.

DR P-PSDB; AD124510.

XX

PT Identifying a candidate Chk1 pathway modulating agent for treating e.g.,

PT cancer, comprises contacting an assay system comprising a MCHK

PT polypeptide or nucleic acid with a test agent and detecting a test agent-

PT biased activity.

XX

XX Example; SEQ ID NO 10; 266bp; English.

XX

CC The present invention describes a method for identifying a candidate Chk1

CC pathway modulating agent. The method comprises: (a) providing an assay

CC system comprising a modifier of Chk1 (MCHK) polypeptide or nucleic acid;

CC (b) contacting the system with a test agent, where the system provides a

CC reference activity except in the presence of the test agent; and (c)

CC detecting a test agent-biased activity, and a difference between the test

CC agent-biased activity and the reference activity. Also described: (1) a

CC method for modulating Chk1 pathway of a cell; (2) a method for modulating

CC Chk1 pathway in a mammalian cell; and (3) a method for diagnosing a

CC disease in a patient. A MCHK sequence has cyostatic activity, and can be

CC used in gene therapy. The method is useful for identifying a candidate

CC Chk1 pathway-modulating agent for preparing a composition for diagnosing

CC or treating e.g., cancer. The present sequence encodes a human MCHK

CC protein, which is used in the exemplification of the present invention.

XX Sequence 993 BP; 203 A; 286 C; 286 G; 221 T; 0 U; 0 Other;

XX Query Match 97.8%; Score 905.2; DB 12; Length 993;

XX Best Local Similarity 99.4%; Pred. No. 2.2e-214;

XX Matches 920; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 4 GCCCATCTGTTTACGACATGCGCAGATCATGAAAGTCGCCAGTGGCAGCACCGCCA 63

Db 68 GCCCATCTGTTTACGACATGCGCAGATCATGAAAGTCGCCAGTGGCAGCACCGCCA 127

QY 64 CCGCGCGCGCGCGCGCGCGCTGCGCGCTGAAAGCGCGCAGACAGAGCGAGCGCGCGCG 123

Db 128 CCGCGCGCGCGCGCGCGCGCTGCGCGCTGAAAGCGCGCAGACAGCAGCGGTGCGGCG 187

QY 124 AGGTGATGCGCTGTCTGTGAGAGAGCGGTGGCATCTGCGCGT---CGGGGCGCG 180

Db 188 AGGTGATGCGCTGTCTGTGAGAGAGCGGTGGCATCTGCGCGT---CGGGGCGCG 247

QY 181 GGGCGCGCTGCGCGCGCTGCGCGCTGAGCAGACAGAGTAAAGTGTCTCTACACATGA 240

Db 248 GGGCGCGCTGCGCGCGCTGCGCGCTGAGCAGACAGAGTAAAGTGTCTCTACACATGA 307

QY 241 ACGGCTGTACTCAGCGCTCAAGAGCGTGGTCCCACTGCGCGCAGAACCGCAAGTGA 300

Db 308 ACGGCTGTACTCAGCGCTCAAGAGCGTGGTCCCACTGCGCGCAGAACCGCAAGTGA 367

QY 301 GCAAGTGAAGATTTCTCAGCAGCTCATGACTATCATCAGAGACCTTCAGTTGAGCTGA 360

Db 368 GCAAGTGAAGATTTCTCAGCAGCTCATGACTATCATCAGAGACCTTCAGTTGAGCTGA 427

QY 361 ACTCGAATCCGAAGTTGGGACCCCGGGGCGGAGGGCTGCCGCTCCGCTCA 420

Db 428 ACTCGAATCCGAAGTTGGGACCCCGGGGCGGAGGGCTGCCGCTCCGCTCA 487

QY 421 GCACCTTCAGCGCGAGATCAGCGCGCTCAAGCGCGAGAGCGGATGCTTCTGCGGACG 480

Db 488 GCACCTTCAGCGCGAGATCAGCGCGCTCAAGCGCGAGAGCGGATGCTTCTGCGGACG 547

QY 481 ATGCACTTGTGTGCTGAGAGCGCTCCCGCAGGACCGGACCGCCAGCATCAGG 540

Db 548 ATGCACTTGTGTGCTGAGAGCGCTCCCGCAGGACCGGACCGCCAGCATCAGG 607

QY 541 GGGCAAGAGAAATTAAGTGTCTGTGGGTCTCCCGCAAGCGCGCTGCGGATCTGAGG 600

Db 608 GGGCAAGAGAAATTAAGTGTCTGTGGGTCTCCCGCAAGCGCGCTGCGGATCTGAGG 667

QY 601 AGAACAAAGCCGATCGCGCGCGCTGCGCGCTTAACTGCATCCAGCTGGGCTGAGGCT 660

Db 668 AGAACAAAGCCGATCGCGCGCGCTGCGCGCTTAACTGCATCCAGCTGGGCTGAGGCT 727

QY 661 GAGGCACTGGCGAGAGAGAGGCGCTCTCTGACACACTACTAGTACACAGACTTGA 720

Db 728 GAGGCACTGGCGAGAGAGAGGCGCTCTCTGACACACTACTAGTACACAGACTTGA 787

QY 721 GGGGATGGGATTCACATCGTGTGTTCTAATTTTGAAGAGACATTTTAAATAATG 780

Db 788 GGGGATGGGATTCACATCGTGTGTTCTAATTTTGAAGAGACATTTTAAATAATG 847

QY 781 TCACGTTGTGTCTCAGATTTCTGAGAAATGCTTTGATGTATTAATACATGAT 840

Db 848 TCACGTTGTGTCTCAGATTTCTGAGAAATGCTTTGATGTATTAATACATGAT 907

QY 841 CACCGACTGAGAAATTTGTTTACAAATAGTTCTGTGGGCTGTTTTTGTATTAAACA 900

Db 908 CACCGACTGAGAAATTTGTTTACAAATAGTTCTGTGGGCTGTTTTTGTATTAAACA 967

QY 901 AATTAATTAGATGTGAAAAAAA 926

Db 968 AATTAATTAGATGTGAAAAAAA 993

RESULT 7  
AAS44963  
ID AAS44963 standard; cDNA; 979 BP.  
XX  
XX AAS44963;

AC AAS44963;

DT 18-DEC-2001 (first entry)

XX cDNA encoding novel human secretory protein, seq ID No 44.

DE Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;

KW ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;

KW transgenic animal; Alzheimer's disease; Parkinson's disease; burn;

KW amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;

ulcer; osteoporosis; bone degenerative disorder; periodontal disease; gut protection; lung; liver fibrosis; immune deficiency; infection; severe combined immunodeficiency; SCID; autoimmune disorder; allergy; multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma; fertility; analgesic; pain; antigen; ss.

Homo sapiens.

MO20016689-A2.

13-SEP-2001.

05-MAR-2001; 2001WO-US004942.

07-MAR-2000; 2000US-00519705.

19-MAY-2000; 2000US-00574454.

17-JUN-2000; 2000US-00596193.

14-JUL-2000; 2000US-00616847.

19-SEP-2000; 2000US-00665363.

20-OCT-2000; 2000US-00693267.

(HSE-) HSEQ INC.

Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P; Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J; MPI: 2001-589934/66. P-PSDB; AAU28063.

Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis and treatment of cancer, neurological, inflammatory, and autoimmune disorders.

Claim 1. SEQ ID NO 44; 107pp; English.

The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune response, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of cerebral and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects biorythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAS44920-AAS45295 represent novel human secreted protein coding sequences of the invention

Sequence 979 BP; 202 A; 277 C; 283 G; 217 T; 0 U; 0 Other;

Query Match 96.9%; Score 897.2; DB 5; Length 979;

Best Local Similarity 98.8%; Pred. No. 2.1e-212;

	Matches	915; Conservative	0; Mismatches	8; Indels	3; Gaps	1;
QY	4	GGCCATTCTGTTTACGCCAGTGGCCAAAGATCATGAAGTGGCCAGTGGACACCGCA				63
Db	52	GGCCATTCTGTTTACGCCAGTGGCCAAAGATCATGAAGTGGCCAGTGGACACCGCA				111
QY	64	CCGCCCGCGGGCCCGCCAGCTGCGCTGAAAGCCGCAAGACAGCGTGGCGGCG				123
Db	112	CCGCCCGCGGGCCCGCCAGCTGCGCTGAAAGCCGCAAGACAGCGTGGCGGCG				171
QY	124	AGTGTGCGCTGTCTGTCTGAGCAGAGCGTGGCCATCTCGCGCTG--CCGGGCGCGG				180
Db	172	AGTGTGCGCTGTCTGTCTGAGCAGAGCGTGGCCATCTCGCGCTGCGCGGGGCGCGG				231
QY	181	GGGGCGCGCTGCTGCTGCTGAGCAGAGCGTAAAGTGTGCTTACGACATGA				240
Db	222	GGGGCGCGCTGCTGCTGCTGAGCAGAGCGTAAAGTGTGCTTACGACATGA				291
QY	241	ACGGCTGTACTCAGCGCTCAAGAGAGTGTGCCACCGTGGCCGCAAGAGTGA				300
Db	292	ACGGCTGTACTCAGCGCTCAAGAGAGTGTGCCACCGTGGCCGCAAGAGTGA				351
QY	301	GCAAGTGAAGATTCTCAGCAGCTCATCTGACTACATCAAGGACCTTCAATTGAGCTGA				360
Db	352	GCAAGTGAAGATTCTCAGCAGCTCATCTGACTACATCAAGGACCTTCAATTGAGCTGA				411
QY	361	ACTCGGAATCCGAATTTGGAGCCCGGGGGCGGAGGCTGGCGGTCGGCTCGCTCA				420
Db	412	ACTCGGAATCCGAATTTGGAGCCCGGGGGCGGAGGCTGGCGGTCGGCTCGCTCA				471
QY	421	GCAACCTCAAGCGCGAGATCAGCGCTGACCGCGAGAGCGGATCGTCTCGGAGCG				480
Db	472	GCAACCTCAAGCGCGAGATCAGCGCTGACCGCGAGAGCGGATCGTCTCGGAGCG				531
QY	481	ATCGCATTTGTGTGTGTGAAGCGGCTTCCCGAGGACCGGAGACCCAGCCATCCAGG				540
Db	532	ATCGCATTTGTGTGTGTGAAGCGGCTTCCCGAGGACCGGAGACCCAGCCATCCAGG				591
QY	541	GGGCAAGAGAAATTACGTGCTTGTGGGTCTCCCAACGCGCTTCGCGGATTCGAGGG				600
Db	592	GGGCAAGAGAAATTACGTGCTTGTGGGTCTCCCAACGCGCTTCGCGGATTCGAGGG				651
QY	601	AGAACAAAGCGATGGGCGGCGCATGCGCCCTTAAGTCAATCAGCTGGGCTGAGGCT				660
Db	652	AGAACAAAGCGATGGGCGGCGCATGCGCCCTTAAGTCAATCAGCTGGGCTGAGGCT				711
QY	661	GAGGCACTGGCGAGAGAGGGGCTCTCTGTGCAACACTACTAGTCAACAGAGACTTGA				720
Db	712	GAGGCACTGGCGAGAGAGGGGCTCTCTGTGCAACACTACTAGTCAACAGAGACTTGA				771
QY	721	GGGGGTGGGATTCACCTGTGTCTTATTTTGGAAAAGGACATTTTAAAAATGG				780
Db	772	GGGGGTGGGATTCACCTGTGTCTTATTTTGGAAAAGGACATTTTAAAAATGG				831
QY	781	TCAGCTTTGGGCTCTCAGATTTCTGAGAAATGCTTGTATGTATATACATGAT				840
Db	832	TCAGCTTTGGGCTCTCAGATTTCTGAGAAATGCTTGTATGTATATACATGAT				891
QY	841	CACCGACTGAGATATTTTATACATATGTTGTGTGGGCTGTTTTTTTATTAACA				900
Db	892	CCCGCAGTGAATAATTTTATACATATGTTGTGTGGGCTGTTTTTTTATTAACA				951
QY	901	AATATTTTATGATGTGAAAAAAA 926				
Db	952	AATATTTTATGATGTGAAAAAAA 977				
RESULT 8						
AAFI8245						
ID	AAFI8245	standard; DNA; 1027 BP.				
XX						
AC	AAFI8245;					
XX						

DT 14-MAR-2001 (first entry)  
XX Lung cancer associated polynucleotide sequence SEQ ID 264.  
DE  
XX Human; lung cancer associated protein; neuroprotective; cytoskeletal;  
KW cathectin; immunomodulatory; muscular active; vulnary;  
KW gastroenteric; nephrotropic; antiinfective; gynecological;  
KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;  
KW proliferative disorder; wound healing; infectious disease; da.  
XX  
OS Homo sapiens.  
PN WO20055180-A2.  
XX  
XX 21-SEP-2000.  
PD  
XX 08-MAR-2000; 2000WO-US005918.  
PF  
XX 12-MAR-1999; 99US-0124270P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
XX  
XX Ruben SM;  
PI  
XX WPI; 2000-587514/55.  
DR P-Psdb; AAB58369.  
DR  
XX Lung cancer associated gene sequences, referred to as lung cancer  
PT antigens, useful for treatment, prevention, and diagnosis of disorders  
PT such as lung cancer.  
XX  
XX  
PS Claim 1; Page 724; 1425pp; English.  
XX  
XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer  
CC associated proteins represented in AAB58106 - AAB58548. Lung cancer  
CC associated proteins and polynucleotide sequences, their agonists, and  
CC immunomodulatory; muscular active general; vulnary; gastroenteric  
CC general; nephrotropic; antiinfective; gynecological; or antibacterial  
CC activity. The invention also includes antibodies specific for the protein  
CC or polynucleotide sequences. The lung cancer associated polynucleotide  
CC sequences may be used for detection of lung cancer, chromosome  
CC identification, as chromosome markers, and for numerous other diagnostic  
CC or research purposes. The proteins may be used to treat disorders such as  
CC neural, immune, muscular, reproductive, gastroenteric, pulmonary,  
CC cardiovascular, renal, and proliferative disorders. The proteins may also  
CC be used in the treatment of wounds and infectious diseases.  
CC Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are  
CC used in the course of the invention for the identification and  
CC characterisation of the polynucleotide and protein sequences  
XX  
SQ Sequence 1027 BP; 227 A; 287 C; 294 G; 219 T; 0 U; 0 Other;  
Query Match 96.5%; Score 893.2; DB 3; Length 1027;  
Best Local Similarity 99.2%; Pred. No. 2.1e-211;  
Matches 919; Conservative 0; Mismatches 3; Indels 4; Gaps 2;

QY 241 ACGGCTGTACTCAAGGAGGCTGAGGCCACCTGCCCCAGAACCGGAGGTGA 300  
DB 314 ACGGCTGTACTCAAGGAGGCTGAGGCCACCTGCCCCAGAACCGGAGGTGA 372  
QY 301 GCAAGGTGAGATTTCTCAGACGCTCATGCACTACATCAGGAGCTTCAAGTTGAGCTGA 360  
DB 373 GCAAGGTGAGATTTCTCAGACGCTCATGCACTACATCAGGAGCTTCAAGTTGAGCTGA 432  
QY 361 ACTGGGAATCCGAAGTTGGGACCCCGGGGGCCGAGGGCTGCGGCTCCGCTCA 420  
DB 433 ACTGGGAATCCGAAGTTGGGACCCCGGGGGCCGAGGGCTGCGGCTCCGCTCA 492  
QY 421 GCACCTCAACGGGAGATGAGCGCCCTGACGCGCGAGGCGGAGCTTCTGCGGAGC 480  
DB 493 GCACCTCAACGGGAGATGAGCGCCCTGACGCGCGAGGCGGAGCTTCTGCGGAGC 552  
QY 481 ATGCGATCTTGTGTGCTGAAAGCGCTCCCGCAGAGACCGGCGGACCCGACATCCAGG 540  
DB 553 ATGCGATCTTGTGTGCTGAAAGCGCTCCCGCAGAGACCGGCGGACCCGACATCCAGG 612  
QY 541 GGGCAAGGAATTAAGTGTCTGTGGGTCTCCCGCAAGCGGCTCGCGGATCTGAGG 600  
DB 613 GGGCAAGGAATTAAGTGTCTGTGGGTCTCCCGCAAGCGGCTCGCGGATCTGAGG 672  
QY 601 AGAACAGAGCCGATCGGCGGCACTGCGCCCTTAATGATCCAGCCGCGGCTGAGGCT 660  
DB 673 AGAACAGAGCCGATCGGCGGCACTGCGCCCTTAATGATCCAGCCGCGGCTGAGGCT 732  
QY 661 GAGGCACTGGGAGAGAGGCGCTCCTCTGCGACACTAGTACCGAGAGCTTTA 720  
DB 733 GAGGCACTGGGAGAGAGGCGCTCCTCTGCGACACTAGTACCGAGAGCTTTA 792  
QY 721 GGGGCTGGGATTCACCTGCTGCTTTCTATTTTGAAGACACATTTTAAAAATG 780  
DB 793 GGGGCTGGGATTCACCTGCTGCTTTCTATTTTGAAGACACATTTTAAAAATG 852  
QY 781 TCACGTTGGGCTTCCAGATTTCTGAGGAATTTGCTTTGATGATATTAATGAT 840  
DB 853 TCACGTTGGGCTTCCAGATTTCTGAGGAATTTGCTTTGATGATATTAATGAT 912  
QY 841 CACCGAGTGAATATTTGTTTCAATAGTCTGTGGGCTGTTTTTTGTTATTAACA 900  
DB 913 CACCGAGTGAATATTTGTTTCAATAGTCTGTGGGCTGTTTTTTGTTATTAACA 972  
QY 901 AATTAATTTAGTGTGAAAAA 926  
DB 973 AATTAATTTAGTGTGAAAAA 998  
RESULT 9  
AA16586  
ID AA16586 standard; cDNA; 4793 BP.  
AC AA16586;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
XX DNA encoding human inhibitor of DNA binding-1.  
DE  
XX Human; inhibitor of DNA binding-1; Id-1; cytoskeletal; antiinflammatory;  
KW immunosuppressive; antisense therapy; antisense oligonucleotide;  
KW hyperproliferative disorder; immune disorder; muscular disorder; ss;  
KW vascular disorder; pancreatic disorder; infection; inflammation; tumour.  
XX  
OS Homo sapiens.  
XX  
XX Key location/Qualifiers  
FH 2210. .2659  
FT /cage= a  
FT /product= "Inhibitor of DNA binding-1"  
XX  
PN WO200183513-A2.

XX 08-NOV-2001.  
PD 25-APR-2001; 2001WO-US013209.  
XX 28-APR-2000; 2000US-00561497.  
XX (ISIS-) ISIS PHARM INC.  
PI Baker BF, Bennett CF, Wyatt JR;  
XX WPI; 2002-041477/05.  
DR P-PSDB; AAU10352.  
XX  
PT Novel antisense compound, specifically hybridizing to and inhibiting the  
PT expression of inhibitor of DNA binding-1, useful for treating  
PT hyperproliferative, immune, muscular, vascular or pancreatic disorder.  
PS  
PS Example 15; Page 89-92; 105pp; English.  
XX  
XX The invention relates to novel antisense compounds (I) 8-30 nucleobases  
CC in length targeted to a nucleic acid molecule encoding inhibitor of DNA  
CC binding-1, where (I) specifically hybridizes with and inhibits the  
CC expression of inhibitor of DNA binding-1. Antisense inhibition of human  
CC inhibitor of DNA binding-1 expression by chimeric phosphorothioate  
CC oligonucleotides having 2'-methoxyethyl (2'-MOE) wings and a decoy gap  
CC was tested. A series of oligonucleotides were designed to target  
CC different regions of the human inhibitor of DNA binding-1 RNA. The  
CC compounds were analysed for their effect on human inhibitor of DNA  
CC binding-1 mRNA levels by quantitative real-time polymerase chain reaction  
CC (PCR). The result showed that the oligonucleotides showed at least 25%  
CC inhibition of human inhibitor of DNA binding-1 expression. (I) is useful  
CC for inhibiting the expression of inhibitor of DNA binding-1 in cells or  
CC tissues by contacting the cells or tissues with (I). (I) is also useful  
CC for treating a human having a disease or condition associated with  
CC inhibitor of DNA binding-1 by administering a therapeutically or  
CC prophylactically effective amount of (I), where the disease or condition  
CC is a hyperproliferative disorder, immune disorder, muscular disorder,  
CC vascular disorder or pancreatic disorder. (I) may also be used for  
CC diagnostics, therapeutics, prophylaxis (e.g., to prevent or delay  
CC infection, inflammation or tumour formation), and as research reagents  
CC and kits. (I) may be safely and effectively administered to humans. The  
CC present sequence represents the coding sequence of human inhibitor of DNA  
CC binding-1, which was used to design the antisense oligonucleotides of the  
CC invention  
XX  
XX Sequence 4793 BP; 1038 A; 1282 C; 1339 G; 1134 T; 0 U; 0 Other;  
SQ  
Query Match 70.0%; Score 648; DB 6; Length 4793;  
Best Local Similarity 78.7%; Pred. No. 2.8e-150;  
Matches 913; Conservative 0; Mismatches 5; Indels 242; Gaps 2;  
QY 4 GCCCATTTCTGTTTACAGCCAGTCCCAAGATCATGAAAGTCGACATGACAGCCGCCA 63  
DB 2178 GCCCATTTCTGTTTACAGCCAGTCCCAAGATCATGAAAGTCGACATGACAGCCGCCA 2237  
QY 64 CCGCCGCCCGGGGCCCGAGTGGCGCTGAAGCCGCGCAAGACAGCGCGTGGCGGCG 123  
DB 2238 CCGCCGCCCGGGGCCCGAGTGGCGCTGAAGCCGCGCAAGACAGCGCGTGGCGGCG 2297  
QY 124 AGGTGGTGGCGCTCTGCTGAGACAGAGTGGCCATCTCCGCGT---CCGGGGGCGCG 180  
DB 2298 AGGTGGTGGCGCTCTGCTGAGACAGAGTGGCCATCTCCGCGTGGCGGGGGGCGCG 2357  
QY 181 GGGCGGCGCTGCTGCTGCTGAGACAGAGTGAACGTCGTCTCTACGACATGA 240  
DB 2358 GGGCGGCGCTGCTGCTGCTGAGACAGAGTGAACGTCGTCTCTACGACATGA 2417  
QY 241 ACCGCTGTTTACTACAGCGCTTCAAGAGAGTGGTCCACACCTGCCCAAGACCGCAAGTGA 300  
DB 2418 ACCGCTGTTTACTACAGCGCTTCAAGAGAGTGGTCCACACCTGCCCAAGACCGCAAGTGA 2477  
QY 301 GCAAGGTGAGATTCTTCAGACGTCATGACTACATCAAGGAGCCTTCAAGTGGAGCTGA 360

DB 2478 GCAAGGTGAGATTCTTCAGACGTCATGACTACATCAAGGAGCCTTCAAGTGGAGCTGA 2537  
QY 361 ACTCGGAATCCGAAGTTGGAGACCCCGGGGGGCGCGAGGGCTCGCGTCCGGCTCA 420  
DB 2538 ACTCGGAATCCGAAGTTGGAGACCCCGGGGGGCGCGAGGGCTCGCGTCCGGCTCA 2597  
QY 421 GCACCTCAAGCGGAGATCAGCGGCTGACGGCGG----- 456  
DB 2598 GCACCTCAAGCGGAGATCAGCGGCTGACGGCGGAGGTGAGATCCAGATCCAGCACT 2657  
QY 457 ----- 456  
DB 2658 AGATCATCTTATACCGACGGGGAACGAGGCGCAGAGAGGGCGTGGACACAC 2717  
QY 457 ----- 456  
DB 2718 TTCGTCCTCCATCTTTCGGGTTACTGCTATGCGGGGTGCTTAAGAGCCTGAAAAAG 2777  
QY 457 ----- 456  
DB 2778 CGCTCCCCCGTCTGCTTCTGCGGAAGGGGCGTTCCGCTGCGTCCGAGCGGCTCCT 2837  
QY 457 ----- AGCGGCGATCGTTCTGCGAGCA 481  
DB 2838 TCCAACCGCGCGTCTCATTTTCTCTCGTTTACAGAGCGGATCGTTCTGCGAGCA 2897  
QY 482 TCGCATCTTGTGCTGCTGAGAGCGCTCCCGCAGGACCGGCGGACCCCAACCATCCAGG 541  
DB 2898 TCGCATCTTGTGCTGCTGAGAGCGCTCCCGCAGGACCGGCGGACCCCAACCATCCAGG 2957  
QY 542 GCGAAGAGAAATTACGTCGTCTGAGGTCCTCCCGAAGCGGCTGCGGATCTAGAGGA 601  
DB 2958 GCGAAGAGAAATTACGTCGTCTGAGGTCCTCCCGAAGCGGCTGCGGATCTAGAGGA 3017  
QY 602 GAACAAGACCGATCCGCGGCGCATCGCCTTAATGATCCAGCTGGGCTGAGGCTG 661  
DB 3018 GAACAAGACCGATCCGCGGCGCATCGCCTTAATGATCCAGCTGGGCTGAGGCTG 3077  
QY 662 AGCACTGGCGAGAGAGGGCGCTCTCTGACACACTTAATGATCCAGAGACTTNG 721  
DB 3078 AGCACTGGCGAGAGAGGGCGCTCTCTGACACACTTAATGATCCAGAGACTTNG 3137  
QY 722 GGGGTGGATTCACATCGTGTCTTCTATTTTGAAGAGACATTTTAAATGAT 781  
DB 3138 GGGGTGGATTCACATCGTGTCTTCTATTTTGAAGAGACATTTTAAATGAT 3197  
QY 782 CACGTTGGTGTCTCAGATTTCTGAGAAATGCTTTGATGATTAATGATC 841  
DB 3198 CACGTTGGTGTCTCAGATTTCTGAGAAATGCTTTGATGATTAATGATC 3257  
QY 842 ACCGACTGAAATATGTTTACAAATAGTCTGAGGGCTGTTTTTGTATTAACAA 901  
DB 3258 ACCGACTGAAATATGTTTACAAATAGTCTGAGGGCTGTTTTTGTATTAACAA 3317  
QY 902 ATTAATTAGATGTGAAAA 921  
DB 3318 ATTAATTAGATGTGTA 3337  
RESULT 10  
AAZ33520  
ID AAZ33520 standard; cDNA; 1216 BP.  
XX  
XX AAZ33520;  
XX  
XX 08-DEC-1999 (first entry)  
XX Human prostate cancer-associated EST 44.  
XX  
XX Expressed sequence tag; EST; prostate; tumor; treatment; gene therapy;  
XX cancer; tissue specificity; human; 86.  
XX

OS Homo sapiens.  
XX DE1981194-A1.  
XX  
PD 16-SEP-1999.  
XX  
PF 10-MAR-1998; 98DE-01011194.  
XX  
PR 10-MAR-1998; 98DE-01011194.  
XX  
PA (META-) METAGEN GES GENOMFORSCHUNG MBH.  
XX  
PI Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;  
XX WPI, 1999-519629/44.  
DR P-PSDB; AAY48404.  
XX  
PT New nucleic acid expressed at high level in normal prostatic tissue and  
XX encoded polypeptides, used to treat cancer and screen for therapeutic  
XX agents.  
PS Claim 3; 109; 194dp; German.  
XX  
CC This invention describes novel nucleic acid sequences (A) that are  
CC expressed at high level in normal prostatic tissue. Polypeptides (I)  
CC encoded by (A) are used: (a) for identifying agents for treatment of  
CC prostatic cancer and (b) for therapy of prostate cancer, optionally where  
CC expressed by gene therapy methods. (A) is also used to isolate full-  
CC length genes (for gene therapy) and for recombinant production of (I),  
CC which can be used to raise specific antibodies. (A) are identified by  
CC assembly of ESTs (expressed sequence tags) before these are analyzed by  
CC expression pattern (tissue specificity). This approach eliminates many of  
CC the false results, as regards tissue specificity, associated with known  
CC methods that use single (usually short) ESTs. AA233477-233540 represent  
CC expressed sequence tags described in the method of the invention  
XX  
SQ Sequence 1216 BP; 248 A; 349 C; 354 G; 265 T; 0 U; 0 Other;  
  
Query Match 67.2%; Score 622; DB 2; Length 1216;  
Best Local Similarity 77.8%; Pred. No. 4,6e-144;  
Matches 904; Conservative 0; Mismatches 15; Indels 243; Gaps 3;  
  
QY 4 GCCCATTTCTGTTTCAAGCCAGTCGCCAAGATCATGAAGTCCGACGTGGACACCGGCA 63  
DB 55 GCCCATTTCTGTTTCAAGCCAGTCGCCAAGATCATGAAGTCCGACGTGGACACCGGCA 114  
QY 64 CCGCCGCGCGCGCGCCAGCTGCGCTGAAGCGCGGCAAGACGCGGTGCGGCG 123  
DB 115 CCGCCGCGCGCGCGCCAGCTGCGCTGAAGCGCGGCAAGACGCGGTGCGGCG 173  
QY 124 AGGTGTCGCTGTCTGTCTGACAGAGCGTGGCATCTCGGCGTCCGCGGCGCGG 183  
DB 174 AGGTGTCGCTGTCTGTCTGACAGAGCGTGGCATCTCGGCGTGAAGGCGG---GCGGG 230  
QY 184 CCGGCGCTGCTGCGCTGTCGACAGAGCGTGAAGAGTAAAGTCTGCTTACGACATGAAG 243  
DB 231 GCACTGCGCTGCGCTGTCGACAGAGCGTGAAGAGTAAAGTCTGCTTACGACATGAAG 290  
QY 244 GCTGTTACTCAGCCTCAAGAGAGTGTGCCACCGTCCGCGGCAAGCGGAGTGCA 303  
DB 291 GCTGTTACTCAGCCTCAAGAGAGTGTGCCACCGTCCGCGGCAAGCGGAGTGCA 350  
QY 304 AGGTGGAATTTCTCAGACGTCATCGATCATCAAGGACCTTCAGTTGAGGCTGAAT 363  
DB 351 AGGTGGAATTTCTCAGACGTCATCGATCATCAAGGACCTTCAGTTGAGGCTGAAT 410  
QY 364 CGGAATCCGAAGTTGGAGCCCGCGGGGCGAGGGGCTGCGGCTCGCTCAGCA 423  
DB 411 CGGAATCCGAAGTTGGAGCCCGCGGGGCGAGGGGCTGCGGCTCGCTCAGCA 470  
QY 424 CCTTCAAGCGGAGATCAGCGCTTGAAGCGGCGG----- 456  
DB 471 CCTTCAAGCGGAGATCAGCGCTTGAAGCGGCGGCGGAGTGAATCAGATCCGACCTAAGA 530

QY 457 ----- 456  
DB 531 TCATCCTTATACCGACGGGGAAACGAGAGCCAGAGAGGCGTGGCGCTTGCACTTC 590  
QY 457 ----- 456  
DB 591 CGTCCCATCTTGGCGGATACCTGGCTATGCGGGGGTGTCTTAAGAGCTTGAAAAAGCGC 650  
QY 457 ----- 456  
DB 651 TCCCGCTGTCGCTTCTGCGGAAAGGGGCGTTCGCTGCGCTGAGACGGCGTCCCTCC 710  
QY 457 -----AGCGGCAATGGCTTCTCTCGGACGATCG 484  
DB 711 AACCGCGCGCTCATTTCTTCTGTTTTCACACAGCGGCAATGGCTTCTCGGACGATCG 770  
QY 485 CATCTTGTGTCTGAAAGCGCTTCCCGAGGAGCCGCGGACCCCAAGCCATCCAGGGGCG 544  
DB 771 CATCTTGTGTCTGAAAGCGCTTCCCGAGGAGCCGCGGACCCCAAGCCATCCAGGGGCG 830  
QY 545 AAGAGAAATTACGTCCTGTCGAGTCCCGGCAAGCGGCTCGCGGATCTGAGGAGAA 604  
DB 831 AAGAGAAATTACGTCCTGTCGAGTCCCGGCAAGCGGCTCGCGGATCTGAGGAGAA 890  
QY 605 CAAGACGATCGCGCGCACTGCGCCCTTAACTGATCCAGCCTGCGGCTGAGGCTGAGG 664  
DB 891 CAAGACGATCGCGCGCACTGCGCCCTTAACTGATCCAGCCTGCGGCTGAGGCTGAGG 950  
QY 665 CACTGCGAGAGAGGGGCGCTCTCTCTGACACCTGATGATGACAGAGACTTTAGGGG 724  
DB 951 CACTGCGAGAGAGGGGCGCTCTCTCTGACACCTGATGATGATGATGATGATGATGATG 1010  
QY 725 GTGGGATTCACCTGTCGTGTCTTATTTTGAAGAGCAGACATTTTAAAAATGTCAC 784  
DB 1011 GTGGGATTCACCTGTCGTGTCTTATTTTGAAGAGCAGACATTTTAAAAATGTCAC 1070  
QY 785 GTTGGGCTTCTGACATTTCTGAGAAATTCCTTGTATGATATTAATGATGATGATGATG 844  
DB 1071 GTTGGGCTTCTGACATTTCTGAGAAATTCCTTGTATGATATTAATGATGATGATGATG 1130  
QY 845 GACTGGAATATTTGTTTACATAGTTCGAGGCGCTGTTTGTATTAATTAACAATA 904  
DB 1131 GACTGGAATATTTGTTTACATAGTTCGAGGCGCTGTTTGTATTAATTAACAATA 1190  
QY 905 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 926  
DB 1191 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1212  
  
RESULT 11  
ID AB283034  
AB283034 standard; cDNA, 682 BP.  
XX  
XX AB283034;  
AC  
AC  
DT 14-MAY-2003 (first entry)  
XX  
XX  
DE Toxicologically relevant human nucleotide sequence #193.  
XX  
XX  
KW Toxicologically relevant gene; toxicological response; gene; ss.  
XX  
XX Homo sapiens.  
PN W02003016500-A2.  
XX  
XX  
PD 27-FEB-2003.  
XX  
XX  
PF 16-AUG-2002; 2002W0-US026514.  
PR 16-AUG-2001; 2001US-0313080P.  
XX  
XX (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.

XX	Netf RE,	Dunn RT,	Adkins K,	Pickett GG,	Kier LD,	Schmeisner K,	
PI	Alen P,						
DR	WPI,	2003-268322/26.					
XX							
PT	Determining a toxicological response to an agent, useful for screening of						
PT	drugs, comprises comparing the expression profile of one or more human						
PT	toxic response genes to a reference gene expression profile indicative of						
PT	toxicity.						
XX							
PS	Claim 1, Page 103; 455pp; English.						
XX							
CC	The present invention describes a method (M1) for determining a						
CC	toxicological response to an agent, which comprises comparing the						
CC	expression profile of one or more human toxic response genes to a						
CC	reference gene expression profile indicative of toxicity, and so						
CC	determining the presence of a toxic response to the agent. Also						
CC	described: (1) an array comprising one or more polynucleotides selected						
CC	from the genes corresponding to the partial sequences given in AB282842						
CC	to AB284767, or their fragments of at least 20 nucleotides, or homologues						
CC	; and (2) determining if a gene putatively identified to be a toxic						
CC	response gene plays a role on toxic response pathways by determining the						
CC	expression profile of the gene after exposure of cells or a human subject						
CC	to a known toxic pharmaceutical or industrial agent, comprising: (a)						
CC	exposing cells to an agent or isolating cells from a human subject who						
CC	was exposed to an agent; (b) obtaining the test gene expression profile						
CC	for a putatively identified toxic response gene after exposure to a known						
CC	toxic pharmaceutical or industrial agent; and (c) comparing the test						
CC	profile to the expression profile of a gene with a similar function or						
CC	comparing the test profile to the expression profile of that gene after						
CC	exposure to other known toxic compounds. The methods are useful for						
CC	predicting and determining toxicological responses on a cellular, organ						
CC	or system level. The arrays comprising the human genes are useful for						
CC	toxicological screening of drugs, pharmaceutical compounds and chemicals						
XX							
XX	Sequence 682 BP, 136 A, 211 C, 212 G, 122 T, 0 U, 1 Other;						
XX							
Query Match	55.1%;	Score 510.6;	DB 10;	Length 682;			
Best Local Similarity	99.2%;	Pred. No. 1.6e-116;					
Matches 513;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0			
QY	225	CTGCTCTACGACATGAAACGGCTGTATTACTACACGCTTCAGAGAGAGTGTGCCACCTCGCCC	284				
DB	83	CTGCTCTACGACATGAAACGGCTGTATTACTACACGCTTCAGAGAGAGTGTGCCACCTCGCCC	142				
QY	285	CAGAACCCGACAGTGAAGCAAGTGAAGATTCTTCACACAGTCACTCACTACAGGAC	344				
DB	143	CAGAACCCGACAGTGAAGCAAGTGAAGATTCTTCACACAGTCACTCACTACAGGAC	202				
QY	345	CTTCAAGTTGAGACTGAATCCGGAATCCGAAGTTGGAGACCCCGGGGGCCGAGGGCTGGCG	404				
DB	203	CTTCAAGTTGAGACTGAATCCGGAATCCGAAGTTGGAGACCCCGGGGGCCGAGGGCTGGCG	262				
QY	405	GTCGCGGCTCGCTCAGCACCTCTCAACGCGAGATACGAGCCCTGACGCGCCGAGCGGCA	464				
DB	263	GTCGCGGCTCGCTCAGCACCTCTCAACGCGAGATACGAGCCCTGACGCGCCGAGCGGCA	322				
QY	465	TGCGTTCTCGCGGAGCATGTCATTGTGTGCTGAAGGCGCTCCCCAGGAGCGGCG	524				
DB	323	TGCGTTCTCGCGGAGCATGTCATTGTGTGCTGAAGGCGCTCCCCAGGAGCGGCG	382				
QY	525	ACCCGAGCATCATCAGGGGGCAAGAGAAATTACGTCGTGTGGGTCTCCCCCAAGCGGC	584				
DB	383	ACCCGAGCATCATCAGGGGGCAAGAGAAATTACGTCGTGTGGGTCTCCCCCAAGCGGC	442				
QY	585	TGCGCGGATCTGAGGAGAAACAAGCCGATCGCGGCGCATGCGCCCTTACATGATCCA	644				
DB	443	TGCGCGGATCTGAGGAGAAACAAGCCGATCGCGGCGCATGCGCCCTTACATGATCCA	502				
QY	645	GCCTGGGCTGAGAGCTGAGAGCATGCGCGAGAGAGGGCGCTCTCTCTGCAACCTACTA	704				
DB	503	GCCTGGGCTGAGAGCTGAGAGCATGCGCGAGAGAGGGCGCTCTCTCTGCAACCTACTA	562				

QY	705	GTCAACGAGACTTTAGGGGGGGGATTCCTCGTG	741
DB	563	GTCAACGAGACTTTAGGGGGGGGATTCCTCGTG	599
RESULT 12			
ID	AAQ66082	standard; CDNA to mRNA; 509 BP.	
XX	AAQ66082		
AC	25-MAR-2003	(revised)	
XX	23-JAN-1995	(first entry)	
DT	Human Id-1H gene.		
XX	myogenic regulatory factors; transcriptional regulatory factors;		
KW	diagnosis; therapy; cell proliferation; antisense therapy; da.		
XX	Homo sapiens.		
OS	Key	Location/Qualifiers	
FH	CDS	22..486	
FT		/*tag= a	
FT		/product= "Id-H1"	
XX	EP60627-A1.		
FN	08-JUN-1994.		
XX	15-NOV-1993;	93EP-00309097.	
PD	13-NOV-1992;	92UP-00328391.	
XX	(SUME ) SUMITOMO ELECTRIC IND CO.		
PA	Oda K, Nakada S, Hara E, Yamaguchi T, Nakamura T, Oka Y;		
XX	Kishimoto T;		
PI	WPI; 1994-177938/22.		
DR	P-Psdb; AAR53710.		
XX	Novel human Id genes - obid. by probing cDNA library of human TIG-1		
PT	fibroblasts with synthetic oligo:nucleotide probes based on mouse Id		
PT	gene's conserved regions.		
XX	Claim 1; Page 10-11; 18pp; English.		
PS	AAQ66082 encodes a novel human Id-1 (Id-H1). Id proteins have myogenic		
XX	regulatory factor activity, suppressing the activity of muscle specific		
CC	genes. 3 mouse Id genes have been identified and previously only Id-H2		
CC	(which corresponds to the mouse Id-2). The 2 human Id genes in the		
CC	specification are derived from the same genetic locus on a genome by		
CC	alternate splicing (see also AAQ66083 - Id-H1'). The expression of the Id		
CC	-H1 and Id-H1' genes specifically varies according to the state of cell		
CC	proliferation, in particular, the acquisition of cell aging and		
CC	permanently proliferating ability. The genes can be used in diagnostic		
CC	probes for determining the state of proliferation and state of		
CC	differentiation in cells. Antisense molecules may be utilized as		
CC	inhibitors of cell proliferation, where the Id molecules act as		
CC	transcriptional regulatory factors. (Updated on 25-MAR-2003 to correct FN		
CC	field.)		
XX	Sequence 509 BP, 91 A, 170 C, 172 G, 76 T, 0 U, 0 Other;		
XX	Query Match	52.9%; Score 490; DB 2; Length 509;	
XX	Best Local Similarity	96.8%; Pred. No. 1.8e-11;	
XX	Matches 504; Conservative 0; Mismatches 5; Indels 1; Gaps 1		
QY	15	TTTACGCCAGTGGCCCAAGATCATGTAAAGTCCGCAATGGCAGACCGCCACCGCCGGG	74
DB	1	TTTACGCCAGTGGCCCAAGATCATGTAAAGTCCGCAATGGCAGACCGCCACCGCCGGG	60



QY 75 GGGCCCAAGCTGCGCGTGAAGGCGGCAAGACAGGACGGTGGCGGCGAGGTGTCGC 134  
 Db 61 GGGCCCAAGCTGCGCGTGAAGGCGGCAAGACAGGACGGTGGCGGCGAGGTGTCGC 120  
 QY 135 TGTCTGTCTGAGCAGAGGCTGTGGCCATCTCGCGCTGCGCGGCGCGCGGCGCTGCT 194  
 Db 121 TGTCTGTCTGAGCAGAGGCTGTGGCCATCTCGCGCTGCGCGGCGCGCGGCGCTGCT 180  
 QY 195 GCGCTGTGAGCAGAGCAGCAGGTTAAAGTGTGTCTTACGATGAACTGCTTACTCA 254  
 Db 181 GCGCTGTGAGCAGAGCAGCAGGTTAAAGTGTGTCTTACGATGAACTGCTTACTCA 240  
 QY 255 GCGCTGAAGAGCTGTGTCGCCACCTGCGCCGAGAACCGCAAGGTGAGCAGGTTGAGT 314  
 Db 241 GCGCTGAAGAGCTGTGTCGCCACCTGCGCCGAGAACCGCAAGGTGAGCAGGTTGAGT 300  
 QY 315 CTCGACGACGTCATCTGACTATCATAGGAGACCTTCACTTGAAGTGAATCTCGAATCGAA 374  
 Db 301 CTCGACGACGTCATCTGACTATCATAGGAGACCTTCACTTGAAGTGAATCTCGAATCGAA 360  
 QY 375 GTTGAGAACCCCGGCGGCGGCGGAGGCTGCGGCTCGGCTCGACACCTCGAACGCGC 434  
 Db 361 GTTGAGAACCCCGGCGGCGGCGGAGGCTGCGGCTCGGCTCGACACCTCGAACGCGC 420  
 QY 435 GAGATCAGCGCGCTGACGCGCCGAGCGGCACTGCGTCTCTGCGAGCATGTCATCTTGTGT 494  
 Db 421 GAGATCAGCGCGCTGACGCGCCGAGCGGCACTGCGTCTCTGCGAGCATGTCATCTTGTGT 480  
 QY 495 CGCTGAAGCGCTGCGCGCGGCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 524  
 Db 481 CGCTGAAG-gccttcccccaaggacggcg 509

RESULT 13

ABV78155  
 ID ABV78155 standard; DNA; 481 BP.  
 AC ABV78155;  
 DT 15-NOV-2002 (first entry)  
 XX Human ID1 DNA SEQ ID NO 39.  
 XX RNA inhibition; dermal; gene expression inhibitor; oncogene; cytostatic;  
 KM viroicide; protozoicide; gene; ds.  
 OS Homo sapiens.  
 XX WO200255693-A2.  
 PN 18-JUL-2002.  
 PD 09-JAN-2002; 2002WO-EP000152.  
 PF 09-JAN-2001; 2001DE-01000586.  
 PR 26-OCT-2001; 2001DE-01005280.  
 PR 29-NOV-2001; 2001DE-01058411.  
 PR 07-DEC-2001; 2001DE-01060151.  
 XX (RIBO-) RIBOPHARMA AG.  
 PA Kreutzer R, Limmer S, Roost S, Hadwiger P;  
 PI WPI; 2002-590671/63.  
 DR Inhibiting expression of target gene, useful e.g. for inhibiting  
 PT oncogenes, by administering double-stranded RNA complementary to the  
 PT target and having an overhang.  
 XX Claim 10; Page 135; 203pp; German.  
 PS The invention relates to inhibiting expression of a target gene (I) in a  
 CC

CC cell by introducing an inhibitory RNA (dermal) having a double-stranded  
 CC structure of at most 49 consecutive bases. At least part of one strand  
 CC (as1) of dermal is complementary to (I) and at least one end of dermal  
 CC has an overhang of 1-4 nucleotides. The method is used to inhibit the  
 CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.  
 CC in humans, also genes in Plasmidium or in viruses or viroids that are  
 CC pathogenic for humans, animals or plants. Introducing an overhang into  
 CC dermal greatly increases effectiveness for inhibiting gene expression,  
 CC both in vivo and in vitro and also increases stability and thus the  
 CC effective concentration inside the cell. The present sequence is that of  
 CC a gene related to the invention

Seq Sequence 481 BP; 92 A; 153 C; 163 G; 73 T; 0 U; 0 Other;

Query Match 50.3%; Score 466; DB 6; Length 481;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-105;  
 Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 ATGAAAGTGGCAGTGGCAGACCGCCACCGCGCGCGCCAGCTGCGCGTGAAG 95  
 Db 1 ATGAAAGTGGCAGTGGCAGACCGCCACCGCGCGCGCCAGCTGCGCGTGAAG 60  
 QY 96 GCGGCAAGACAGGACCGGTGCGGCGGAGTGTGCTGTCTGAGCAGACGTG 155  
 Db 61 GCGGCAAGACAGGACCGGTGCGGCGGAGTGTGCTGTCTGAGCAGACGTG 120  
 QY 156 GCCATCTCGCGTCCGCGGCGCGCGGCGCGCGCTGCTGCTGTGAGCAGACGNG 215  
 Db 121 GCCATCTCGCGTCCGCGGCGCGCGGCGCGCGCTGCTGCTGTGAGCAGACGNG 180  
 QY 216 GTAAAGTGTGCTTACGATGAAAGCTGTACTACGCTTCAAGAGCTGTGCCC 275  
 Db 181 GTAAAGTGTGCTTACGATGAAAGCTGTACTACGCTTCAAGAGCTGTGCCC 240  
 QY 276 ACCCTGCGCGAAGCGAAGGTGAGCAGTGAATCTCCAGACGCTGATGATG 335  
 Db 241 ACCCTGCGCGAAGCGAAGGTGAGCAGTGAATCTCCAGACGCTGATGATG 300  
 QY 336 ATCAGGAGCCTTCACTGAGTGAAGCTGAACTCGAATCGAAGTTGGAGCCCGGCGGCG 395  
 Db 301 ATCAGGAGCCTTCACTGAGTGAAGCTGAACTCGAATCGAAGTTGGAGCCCGGCGGCG 360  
 QY 396 GGGCTCGGATCGGCGCTCGCTCAGACCCCTCAACCGCGAGATAGCGCCCTGA 455  
 Db 361 GGGCTCGGATCGGCGCTCGCTCAGACCCCTCAACCGCGAGATAGCGCCCTGA 420  
 QY 456 GAGGCGCATGCGTCTCTGCGAGCAGATCGCATCTTGTGCTGCTGA 501  
 Db 421 GAGGCGCATGCGTCTCTGCGAGCAGATCGCATCTTGTGCTGCTGA 466

RESULT 14

ABZ35731  
 ID ABZ35731 standard; DNA; 481 BP.  
 AC ABZ35731;  
 DT 07-FEB-2003 (first entry)  
 XX Human ID1 polynucleotide SEQ ID NO 39.  
 XX Double stranded RNA; dermal; RNAi; RNA inhibition; cytostatic; viroicide;  
 KW protozoicide; gene expression; antitumor; infection; Plasmidium;  
 KW Hepatitis C virus; human papilloma virus; gene; ds.  
 OS Homo sapiens.  
 XX DE10100588-A1.  
 PN 18-JUL-2002.  
 PD 09-JAN-2001; 2001DE-01000588.  
 PF





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QY      336 ATCAGGAGACCTTCAAGTTGAGGCTGAACTCGGAATCCGAAGTTGGGACCCCGGGGGCCGA 395
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Db      301 ATCAGGAGACCTTCAAGTTGAGGCTGAACTCGGAATCCGAAGTTGGGACCCCGGGGGCCGA 360
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QY      396 GGGCTGCCGATCCGGGCTCCGCTCAGCACCTCAACGGCGAGATCAGGCGCCCTGACGGCC 455
      |||
Db      361 GGGCTGCCGATCCGGGCTCCGCTCAGCACCTCAACGGCGAGATCAGGCGCCCTGACGGCC 420
      |||
QY      456 GAGGCGGCGATGCGTTCCTGCGGAGCGATCGCATCTTGTGTGCTGAA 501
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Db      421 GAGGCGGCGATGCGTTCCTGCGGAGCGATCGCATCTTGTGTGCTGAA 466
      |||

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Search completed: December 18, 2004, 15:33:51  
 Job time : 516.452 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2004, 15:09:16 ; Search time 544.117 Seconds  
(without alignments)  
9395.574 Million cell updates/sec

Title: US-09-996-529A-4

Perfect score: 926  
Sequence: 1 ggggcccatctgtttcagc.....ttagatggtgtaaaaaaaaaa 926

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4093002 seqs, 2760418825 residues

Total number of hits satisfying chosen parameters: 8186004

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing first 45 summaries

Published Applications NA:\*

- 1: /cgn2\_6/prodataa2/pubnpa/us07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/prodataa2/pubnpa/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/prodataa2/pubnpa/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/prodataa2/pubnpa/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/prodataa2/pubnpa/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/prodataa2/pubnpa/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/prodataa2/pubnpa/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/prodataa2/pubnpa/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/prodataa2/pubnpa/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/prodataa2/pubnpa/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/prodataa2/pubnpa/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/prodataa2/pubnpa/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/prodataa2/pubnpa/US10A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/prodataa2/pubnpa/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/prodataa2/pubnpa/US10C\_PUBCOMB.seq:\*
- 16: /cgn2\_6/prodataa2/pubnpa/US10D\_PUBCOMB.seq:\*
- 17: /cgn2\_6/prodataa2/pubnpa/US10E\_PUBCOMB.seq:\*
- 18: /cgn2\_6/prodataa2/pubnpa/US10\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/prodataa2/pubnpa/US11\_NEW\_PUB.seq:\*
- 20: /cgn2\_6/prodataa2/pubnpa/US60\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/prodataa2/pubnpa/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	926	100.0	926	15	US-10-388-360-311	Sequence 311, App1
2	926	100.0	926	17	US-10-775-169-143	Sequence 143, App1
3	897.2	96.9	979	15	US-10-291-172-44	Sequence 44, App1
4	897.2	96.9	979	16	US-10-221-278-44	Sequence 44, App1
5	897.2	96.5	1162	15	US-10-119-428-47	Sequence 47, App1
6	893.2	96.5	1027	9	US-09-925-302-264	Sequence 264, App1
7	893.2	96.5	1027	10	US-09-925-302-264	Sequence 264, App1
8	466	50.3	481	17	US-10-384-335C-39	Sequence 39, App1
9	443.6	47.8	958	16	US-10-453-351-1	Sequence 1, App1
10	442.2	47.8	721	9	US-09-835-992A-30	Sequence 30, App1
11	364.8	39.4	663	13	US-10-027-633-116A1	Sequence 116A1, App1
12	364.8	39.4	663	15	US-10-027-633-116A1	Sequence 116A1, App1

13	433.4	37.1	1049	15	US-10-221-172-420	Sequence 420, App
14	343.4	37.1	1049	16	US-10-221-378-420	Sequence 420, App
C 15	341.6	36.9	461	9	US-09-835-992A-31	Sequence 31, Appl
16	289	31.2	1124	9	US-09-911-800A-1574	Sequence 1574, Ap
17	289	31.2	1124	16	US-10-368-934-206	Sequence 206, App
18	284	30.7	326	16	US-10-242-535A-3578	Sequence 3578, App
19	284	30.7	326	16	US-10-085-783A-3578	Sequence 3578, App
20	271.4	29.3	630	16	US-10-404-460-92	Sequence 92, Appl
21	271.4	29.3	285	17	US-10-775-169-90	Sequence 300, Appl
22	269	29.0	1553	17	US-10-433-793-175	Sequence 175, Appl
C 23	268.2	29.0	1553	17	US-10-433-793-176	Sequence 176, Appl
24	255.4	27.6	319	9	US-09-925-299-405	Sequence 405, App
25	255.4	27.6	319	10	US-09-925-299-405	Sequence 405, App
26	230.4	24.9	402	9	US-09-833-381-1304	Sequence 1304, Ap
27	219.4	23.7	256	9	US-09-920-455-34	Sequence 34, Appl
28	216.8	23.4	265	9	US-09-920-455-17	Sequence 17, Appl
29	210.4	22.7	217	9	US-09-920-455-89	Sequence 89, Appl
30	207.2	22.4	224	9	US-09-920-455-180	Sequence 180, App
31	207.2	22.4	224	9	US-09-920-455-181	Sequence 181, App
32	205.4	22.2	213	9	US-09-920-455-95	Sequence 95, Appl
33	199.4	21.5	201	9	US-09-920-455-95	Sequence 95, Appl
34	197.4	21.3	378	9	US-09-960-352-13829	Sequence 1829, A
35	147	15.9	147	16	US-10-453-351-2	Sequence 2, Appl1
36	142.6	15.4	556	18	US-10-363-445A-30861	Sequence 30861, A
C 37	142.6	15.4	556	18	US-10-363-445A-30862	Sequence 30862, A
C 38	135.8	14.7	556	18	US-10-363-445A-30863	Sequence 30863, A
C 39	135.8	14.7	556	18	US-10-363-445A-30864	Sequence 30864, A
C 40	112.8	12.2	556	18	US-10-363-445A-26981	Sequence 26981, A
C 41	112.8	12.2	556	18	US-10-363-445A-26982	Sequence 26982, A
42	111.2	12.0	556	18	US-10-363-445A-26983	Sequence 26983, A
C 43	111.2	12.0	556	18	US-10-363-445A-26984	Sequence 26984, A
C 44	110.6	11.9	2511	10	US-09-764-872-494	Sequence 494, App
45	107.2	11.6	530	9	US-09-919-580-165	Sequence 165, App

## ALIGNMENTS

```

RESULT 1
US-10-388-360-311
: Sequence 311, Application US/10388360
Publication No. US2003022528A1
GENERAL INFORMATION:
APPLICANT: GENOMIC HEALTH
APPLICANT: Baker, Joëlle B.
APPLICANT: Cronin, Maureen T.
APPLICANT: Kiefer, Michael C.
APPLICANT: Shak, Steve
APPLICANT: Walker, Michael Graham
TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSED TUMOR TISSUES
FILE REFERENCE: 39740-0001US
CURRENT APPLICATION NUMBER: US/10/388,360
CURRENT FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 60/412,049
PRIOR FILING DATE: 2002-09-18
PRIOR APPLICATION NUMBER: US 60/364,890
PRIOR FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 384
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 311
LENGTH: 926
TYPE: DNA
ORGANISM: Homo sapiens
US-10-388-360-311

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Query Match	100.0%	Score 926	DB 15	Length 926
Best Local Similarity	100.0%	Pred. No. 6e-259		
Matches	926	Conservative	0	Mismatches 0; Indels 0; Gaps 0

  

Oy	1	GGGGCCCATTCCTGTTTCACCGAGTGGCCCAAGAAATCATTAAGTCGCCAGGTGGCAGCACCG	60
Db	1	GGGGCCCATTCCTGTTTCACCGAGTGGCCCAAGATATATAAAGTCGCCAGGTGGCAGCACCG	60

QY 61 CCACCGCCGCGCGGCGCCGAGCTGGCGCTGAAGGCGCGCAAGACAGCGGCTCGG 120  
DB 61 CCACCGCGCGCGCGGCGCCGAGCTGGCGCTGAAGGCGCGCAAGACAGCGGCTCGG 120  
QY 121 GCGAGGTGGTGGCTGTCTGTCTGTAGAGCAGAGCGTGGCCATCTCGCGCTGCGGGGCGCG 180  
DB 121 GCGAGGTGGTGGCTGTCTGTCTGTAGAGCAGAGCGTGGCCATCTCGCGCTGCGGGGCGCG 180  
QY 181 GGGCGCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 240  
DB 181 GGGCGCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 240  
QY 241 ACAGCTGTACTCAGCGCTCAGAGAGCTGGTGGCCACCTCGCCCAAGAACCGGAAGTGA 300  
DB 241 ACAGCTGTACTCAGCGCTCAGAGAGCTGGTGGCCACCTCGCCCAAGAACCGGAAGTGA 300  
QY 301 GCAAGGTGGAGATTTCTCAGAGAGCTCATTCATCATCAGAGAGCTTTCAGTGGAGCTGA 360  
DB 301 GCAAGGTGGAGATTTCTCAGAGAGCTCATTCATCATCAGAGAGCTTTCAGTGGAGCTGA 360  
QY 361 ACTGGGAATCCGAGTGGGAGCCCGCGGGGCGAGGGGCTGGCGTCCGGGCTCGCTCA 420  
DB 361 ACTGGGAATCCGAGTGGGAGCCCGCGGGGCGAGGGGCTGGCGTCCGGGCTCGCTCA 420  
QY 421 GCACCTCAGACGCGAGATCAGCGCCCTGAAGCGGCGAGGCGGATCGTTCCTGCGAGG 480  
DB 421 GCACCTCAGACGCGAGATCAGCGCCCTGAAGCGGCGAGGCGGATCGTTCCTGCGAGG 480  
QY 481 ATCGCATCTGTGTGCTGAGAGGCGCTCCCGCAAGGAGACCGGCGAGACCCAGCATCCAG 540  
DB 481 ATCGCATCTGTGTGCTGAGAGGCGCTCCCGCAAGGAGACCGGCGAGACCCAGCATCCAG 540  
QY 541 GGGCAAGAGGAATTAAGT 600  
DB 541 GGGCAAGAGGAATTAAGT 600  
QY 601 AGAACAAGACCGATCGGCGGCGCACTGGCGCCCTTAAGTGCATCAGCTGGGCTGAGGCT 660  
DB 601 AGAACAAGACCGATCGGCGGCGCACTGGCGCCCTTAAGTGCATCAGCTGGGCTGAGGCT 660  
QY 661 GAGGCACTGGCGAGAGAGAGGCGCTCTCTCTGCAACCTACTAGTCAACAGAGCTTTA 720  
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QY 721 GGGGGTGGGATTCACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780  
DB 721 GGGGGTGGGATTCACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780  
QY 781 TCACGTTTGTGCTTCTCAGATTTCTGAGAGAAATGCTTTGTATGTATATATATATATAT 840  
DB 781 TCACGTTTGTGCTTCTCAGATTTCTGAGAGAAATGCTTTGTATGTATATATATATATAT 840  
QY 841 CACCGACTGAGAAATTTGTTTAAATAGTTCTGTGGGCTGTTTTTTTGTATTAACA 900  
DB 841 CACCGACTGAGAAATTTGTTTAAATAGTTCTGTGGGCTGTTTTTTTGTATTAACA 900

## RESULT 2

US-10-775-169-143  
Sequence 143, Application US/10775169  
GENERAL INFORMATION:  
APPLICANT: Wyeth  
APPLICANT: Burczynski, Michael  
APPLICANT: Twine, Natalie  
APPLICANT: Dorne, Andrew  
APPLICANT: Trepicchio, William  
TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo  
FILE REFERENCE: AM101080 (031896-013000)

CURRENT APPLICATION NUMBER: US/10/775,169  
BEST FILING DATE: 2004-02-11  
NUMBER OF SEQ ID NOS: 5278  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 143  
LENGTH: 926  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-775-169-143

Query Match 100.0%; Score 926; DB 17; Length 926;  
Best Local Similarity 100.0%; Pred. No. 66-259;  
Matches 926; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGCCCCATTTCTGTTTGAAGCAGTCCGCAAGATCATGAAGTCCGAGTGGACGCG 60  
DB 1 GGGGCCCCATTTCTGTTTGAAGCAGTCCGCAAGATCATGAAGTCCGAGTGGACGCG 60  
QY 61 CCACCGCGCGCGGCGCCCGAGCTGCGCTGAAGGCGCGCAAGAGAGGCGGCGCG 120  
DB 61 CCACCGCGCGCGGCGCCCGAGCTGCGCTGAAGGCGCGCAAGAGAGGCGGCGCG 120  
QY 121 GCGAGGTGGTGGCTGTCTGTCTGTAGAGAGCTGGCCATCTTCGCTCGGCGCGCG 180  
DB 121 GCGAGGTGGTGGCTGTCTGTCTGTAGAGAGCTGGCCATCTTCGCTCGGCGCGCG 180  
QY 181 GGGCGCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 240  
DB 181 GGGCGCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 240  
QY 241 ACAGCTGTACTCAGCGCTCAGAGAGCTGGTGGCCACCTCGCCCAAGAACCGGAAGTGA 300  
DB 241 ACAGCTGTACTCAGCGCTCAGAGAGCTGGTGGCCACCTCGCCCAAGAACCGGAAGTGA 300  
QY 301 GCAAGGTGGAGATTTCTCAGAGAGCTCATTCATCATCAGAGAGCTTTCAGTGGAGCTGA 360  
DB 301 GCAAGGTGGAGATTTCTCAGAGAGCTCATTCATCATCAGAGAGCTTTCAGTGGAGCTGA 360  
QY 361 ACTGGGAATCCGAGTGGGAGCCCGCGGGGCGAGGGGCTGGCGTCCGGGCTCGCTCA 420  
DB 361 ACTGGGAATCCGAGTGGGAGCCCGCGGGGCGAGGGGCTGGCGTCCGGGCTCGCTCA 420  
QY 421 GCACCTCAGACGCGAGATCAGCGCCCTGAAGCGGCGGAGCGGCGGATCGTTCCTGCGAGG 480  
DB 421 GCACCTCAGACGCGAGATCAGCGCCCTGAAGCGGCGGAGCGGCGGATCGTTCCTGCGAGG 480  
QY 481 ATCGCATCTGTGTGCTGAGAGGCGCTCCCGCAAGGAGACCGGCGGACCCAGCATCCAG 540  
DB 481 ATCGCATCTGTGTGCTGAGAGGCGCTCCCGCAAGGAGACCGGCGGACCCAGCATCCAG 540  
QY 541 GGGCAAGAGGAATTAAGT 600  
DB 541 GGGCAAGAGGAATTAAGT 600  
QY 601 AGAACAAGACCGATCGGCGGCGCACTGGCGCCCTTAAGTGCATCAGCTGGGCTGAGGCT 660  
DB 601 AGAACAAGACCGATCGGCGGCGCACTGGCGCCCTTAAGTGCATCAGCTGGGCTGAGGCT 660  
QY 661 GAGGCACTGGCGAGAGAGAGGCGCTCTCTCTGCAACCTACTAGTCAACAGAGCTTTA 720  
DB 661 GAGGCACTGGCGAGAGAGAGGCGCTCTCTCTGCAACCTACTAGTCAACAGAGCTTTA 720  
QY 721 GGGGGTGGGATTCACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780  
DB 721 GGGGGTGGGATTCACCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780  
QY 781 TCACGTTTGTGCTTCTCAGATTTCTGAGAGAAATGCTTTGTATGTATATATATATATAT 840  
DB 781 TCACGTTTGTGCTTCTCAGATTTCTGAGAGAAATGCTTTGTATGTATATATATATATAT 840  
QY 841 CACCGACTGAGAAATTTGTTTAAATAGTTCTGTGGGCTGTTTTTTTGTATTAACA 900  
DB 841 CACCGACTGAGAAATTTGTTTAAATAGTTCTGTGGGCTGTTTTTTTGTATTAACA 900

QY 901 AATAATTAGATGTGAAAAA 926  
Db 901 AATAATTAGATGTGAAAAA 926

RESULT 3  
US-10-291-172-44  
; Sequence 44, Application US/10291172  
; Publication No. US20030228584A1  
; GENERAL INFORMATION:  
; APPLICANT: HySeq, Inc  
; TITLE OF INVENTION: No. US20030228584A1e1 Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-045  
; CURRENT APPLICATION NUMBER: US/10/291,172  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 09/693,267  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/665,363  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 09/616,847  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 09/596,193  
; PRIOR FILING DATE: 2000-06-17  
; PRIOR APPLICATION NUMBER: 09/574,454  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: 09/519,705  
; PRIOR FILING DATE: 2000-03-07  
; NUMBER OF SEQ ID NOS: 752  
; SEQ ID NO 44  
; LENGTH: 979  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (84)..(548)  
US-10-291-172-44

Query Match 96.9%; Score 897.2; DB 15; Length 979;  
Best Local Similarity 98.8%; Pred. No. 1.5e-250;  
Matches 915; Conservative 0; Mismatches 8; Indels 3; Gaps 1;

QY 4 GCCCATTCGTTTCCAGCCAGTGCAGCAAGATCATGAATGCCAGTGCAGACCGCA 63  
Db 52 GCCCATTCGTTTCCAGCCAGTGCAGCAAGATCATGAATGCCAGTGCAGACCGCA 111

QY 64 CCG 123  
Db 112 CCG 171

QY 124 AGGTGGTGGT 180  
Db 172 AGGTGGTGGT 231

QY 181 GGGCG 240  
Db 232 GGGCG 291

QY 241 AGCGGTGTACTCAGCGCTCAAGAGCTGTGCGCCAGTGCAGCAAGTGCAGCAAGTGA 300  
Db 293 AGCGGTGTACTCAGCGCTCAAGAGCTGTGCGCCAGTGCAGCAAGTGCAGCAAGTGA 351

QY 301 GCAAGGTGAGATTCTCAGCAAGTGTGATGATCATCATCAAGGAGCCTTCAGTTGAGCTGA 360  
Db 352 GCAAGGTGAGATTCTCAGCAAGTGTGATGATCATCATCAAGGAGCCTTCAGTTGAGCTGA 411

QY 361 ACTCGGAATCCGAAGTTGGAGCCCCGGGGGCGAGAGGCTGCGGTCGGGCTCCGCTCA 420  
Db 412 ACTCGGAATCCGAAGTTGGAGCCCCGGGGGCGAGAGGCTGCGGTCGGGCTCCGCTCA 471

QY 421 GCACCTCAACGGCGAGATCAGCGCCTGTGACGGCGAGGCGAGGCTGTTCTTGCGAGCG 480  
Db 472 GCACCTCAACGGCGAGATCAGCGCCTGTGACGGCGAGGCGAGGCTGTTCTTGCGAGCG 531

QY 481 ATCGCATCTGTGTCGTGAAGCGCTCCCGAGGGAGCCGGCGAGCCCGACCATTCAGG 540  
Db 532 ATCGCATCTGTGTCGTGAAGCGCTCCCGAGGGAGCCGGCGAGCCCGACCATTCAGG 591

QY 541 GGGCAAGAGAAATTACGTGCTCTGTGGGTCTCCCGCAACGCGCTTCCGCGATTCGAGGG 600  
Db 592 GGGCAAGAGAAATTACGTGCTCTGTGGGTCTCCCGCAACGCGCTTCCGCGATTCGAGGG 651

QY 601 AGAACAAAGCCGATCGCGGCCACCTGCGCCCTTAATCTGATTCAGCTGGGGCTGAGGCT 660  
Db 652 AGAACAAAGCCGATCGCGGCCACCTGCGCCCTTAATCTGATTCAGCTGGGGCTGAGGCT 711

QY 661 GAGGACCTGGGAGAGAGAGGGGCGCTCTCTGCAACCTACTAGTCAACGAGACTTGA 720  
Db 712 GAGGACCTGGGAGAGAGAGGGGCGCTCTCTGCAACCTACTAGTCAACGAGACTTGA 771

QY 721 GGGGGTGGGATTCCTCCTGCTGTGTTTCTAATTTTGAAGAGACATTTTAAAAATGG 780  
Db 772 GGGGGTGGGATTCCTCCTGCTGTGTTTCTAATTTTGAAGAGACATTTTAAAAATGG 831

QY 781 TCACGTTTGGCTTCTCAGATTCTGAGAAATTCCTTTGTATTGTATTAATGAT 840  
Db 832 TCACGTTTGGCTTCTCAGATTCTGAGAAATTCCTTTGTATTGTATTAATGAT 891

QY 841 CACGACTGAAGAAATTTGTTTACAATAGTTCTGTGGGGCTTTTTTTGTTATTAACA 900  
Db 892 CACGACTGAAGAAATTTGTTTACAATAGTTCTGTGGGGCTTTTTTTGTTATTAACA 951

QY 901 AATAATTAGATGTGAAAAA 926  
Db 952 AATAATTAGATGTGAAAAA 977

RESULT 4  
US-10-221-278-44  
; Sequence 44, Application US/10221278  
; Publication No. US20040034208A1  
; GENERAL INFORMATION:  
; APPLICANT: HySeq, Inc  
; TITLE OF INVENTION: No. US20040034208A1e1 Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-045  
; CURRENT APPLICATION NUMBER: US/10/221,278  
; PRIOR FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: 09/693,267  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/665,363  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 09/616,847  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 09/596,193  
; PRIOR FILING DATE: 2000-06-17  
; PRIOR APPLICATION NUMBER: 09/574,454  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: 09/519,705  
; PRIOR FILING DATE: 2000-03-07  
; NUMBER OF SEQ ID NOS: 752  
; SEQ ID NO 44  
; LENGTH: 979  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (84)..(548)  
US-10-221-278-44

Query Match 96.9%; Score 897.2; DB 16; Length 979;  
Best Local Similarity 98.8%; Pred. No. 1.5e-250;  
Matches 915; Conservative 0; Mismatches 8; Indels 3; Gaps 1;

QY 4 GCCCATTCGTTTCCAGCCAGTGCAGCAAGATCATGAATGCCAGTGCAGACCGCA 63  
Db 52 GCCCATTCGTTTCCAGCCAGTGCAGCAAGATCATGAATGCCAGTGCAGACCGCA 111

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QY 64 CCGCGCCGCGGCGCCGAGCTGCGCGCTGAAGGCGCGGCAAGACAGCGAGCGGTGCGGCG 123
Db 112 CCGCGCGCGCGGCGCCGAGCTGCGCGCTGAAGGCGCGGCAAGACAGCGAGCGGTGCGGCG 171
QY 124 AGGTGTGTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
Db 172 AGGTGTGTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 231
QY 181 GGGGCGCGCTGCGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Db 232 GGGGCGCGCGCTGCGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 291
QY 241 ACCGCTGTATCTACGCGCTCAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
Db 292 ACCGCTGTATCTACGCGCTCAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 351
QY 301 GCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
Db 352 GCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 411
QY 361 ACTCGGAATCCGAAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Db 412 ACTCGGAATCCGAAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 471
QY 421 GCACCTCTCAACGCGCGAGATCAGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Db 472 GCACCTCTCAACGCGCGAGATCAGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 531
QY 481 ATGCGATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
Db 532 ATGCGATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 591
QY 541 GGGCAAGAGAAATTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Db 592 GGGCAAGAGAAATTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 651
QY 601 AGAAGAAAGCCGATCGCGCGCGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
Db 652 AGAAGAAAGCCGATCGCGCGCGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 711
QY 661 GAGGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 712 GAGGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 771
QY 721 GGGGGTGGGATTCACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
Db 772 GGGGGTGGGATTCACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 831
QY 781 TCAGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db 832 TCAGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 891
QY 841 CACCGACTGAGAAATTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Db 892 CACCGACTGAGAAATTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 951
QY 901 AATTAATTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 926
Db 952 AATTAATTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 977
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RESULT 5  
US-10-119-428-47

Sequence 47, Application US/10119428  
Publication No. US2003016581A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom  
APPLICANT: Liu, Chenghua  
APPLICANT: Asundi, Vinod  
APPLICANT: Xu, Chongjun  
APPLICANT: Wehtman, Tom  
APPLICANT: Ren, Feiyan

```
APPLICANT: Ma, Yunding  
APPLICANT: Zhou, Ping  
APPLICANT: Zhao, Qing A.  
APPLICANT: Yang, Yonglong  
APPLICANT: Drenth, Radoje T.  
TITLE OF INVENTION: No. US2003016581A1 Nucleic Acids and  
TITLE OF INVENTION: Polypeptides  
FILE REFERENCE: 789CIP2  
CURRENT APPLICATION NUMBER: US/10/119, 428  
CURRENT FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 09/519, 705  
PRIOR FILING DATE: 2000-03-07  
NUMBER OF SEQ ID NOS: 55  
SOFTWARE: PF_genes Version 1.0  
SEQ ID NO 47  
LENGTH: 1162  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURES:  
NAME/KEY: CDS  
LOCATION: (267)..(734)  
FEATURE:  
NAME/KEY: misc_feature  
LOCATION: (1)..(1162)  
OTHER INFORMATION: n = a, t, c or g  
US-10-119-428-47
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Query Match 96.9%; Score 897.2; DB 15; Length 1162;  
Best Local Similarity 98.8%; Prid. No. 1.7e-250;

Matches 915; Conservative 0; Mismatches 8; Indels 3; Gaps 1;

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QY 4 GCCATTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 63
Db 235 GCCATTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 294
QY 64 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 123
Db 295 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 354
QY 124 AGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
Db 355 AGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 414
QY 181 GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Db 415 GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 474
QY 241 AGCGCTGTATCTACGCGCTCAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
Db 475 AGCGCTGTATCTACGCGCTCAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 534
QY 301 GCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
Db 535 GCAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 594
QY 361 ACTCGGAATCCGAAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Db 595 ACTCGGAATCCGAAGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 654
QY 421 GCACCTCTCAACGCGCGAGATCAGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Db 655 GCACCTCTCAACGCGCGAGATCAGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 714
QY 481 ATGCGATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
Db 715 ATGCGATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 774
QY 541 GGGCAAGAGAAATTACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
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Db 775 GGGCAAGAGAAATTAATGCTGTGTGTGGGTCTCCCAACGCGCTCGCGGATCTGAAGG 834  
Qy 601 AGAACAAGACCGATGGGGGCGGACCTGCGCCCTTAATCTGATCTACCTGGGGCTAGGCT 660  
Db 835 AGAACAAGACCGATGGGGGCGGACCTGCGCCCTTAATCTGATCTACCTGGGGCTAGGCT 894  
Qy 661 GAGGCACTGGGAGGAGGAGGCGGCTCCTCTGCAACCTACTATCTACCGAGACTTTA 720  
Db 895 GAGGCACTGGGAGGAGGAGGCGGCTCCTCTGCAACCTACTATCTACCGAGACTTTA 954  
Qy 721 GGGGGTGGGATTCACCTCGTGTGTTCTAATTTTGAAGAAGACATTTTAAAAATGG 780  
Db 955 GGGGGTGGGATTCACCTCGTGTGTTCTAATTTTGAAGAAGACATTTTAAAAATGG 1014  
Qy 781 TCACGTTGGTGTCTCTGATGATTTCTGAGAAATGCTTTGATGTATATTAACATGAT 840  
Db 1015 TCACGTTGGTGTCTCTGATGATTTCTGAGAAATGCTTTGATGTATATTAACATGAT 1074  
Qy 841 CACCGACTGAGAAATGTTTGTACAAATGTTCTGTTGGGGCTGTTTTTGTATTAAACA 900  
Db 1075 CCGGCACTGAAATAATGTTTGTACAAATGTTCTGTGGGGCTGTTTTTGTATTAAACA 1134  
Qy 901 AATAATTTAGATGTGTAATAAAAAA 926  
Db 1135 AATAATTTAGATGTGTAATAAAAAA 1160

RESULT 6  
US-09-925-302-264  
; Sequence 264, Application US/09925302  
; Patent No. US20020044941A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 264  
; LENGTH: 1027  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-302-264

Query Match 96.5%; Score 893.2; DB 9; Length 1027;  
Best Local Similarity 99.2%; Pred. No. 2,3e-249;  
Matches 919; Conservative 0; Mismatches 3; Indels 4; Gaps 2;  
Qy 4 GCCCATTCGTTTCAAGCCAGTCGCCAAGATCATGAAGTCCGACGTGGCAGACCGCA 63  
Db 74 GCCCATTCGTTTCAAGCCAGTCGCCAAGATCATGAAGTCCGACGTGGCAGACCGCA 133  
Qy 64 CCGCCGCGCGGGGCCCAAGTCGCGCTGAAGCGCGGCAAGACAGCGAGCGTGCAGCG 123  
Db 134 CCGCCGCGCGGGGCCCAAGTCGCGCTGAAGCGCGGCAAGACAGCGAGCGTGCAGCG 193  
Qy 124 AGGTGGTGGCTGTCTGTCTGAGCAGAGCGTGGCCATCTCGCGCTG--CCGGGGCGCG 180  
Db 194 AGGTGGTGGCTGTCTGTCTGAGCAGAGCGTGGCCATCTCGCGCTGCGCGGGGGCGCG 253  
Qy 181 GGGCGCGCTGCTGCTGCTGCTGAGACAGACAGGTAAACGTGCTCTACGACATGA 240  
Db 254 GGGCGCGCTGCTGCTGCTGCTGAGACAGACAGGTAAACGTGCTCTACGACATGA 313  
Qy 241 ACGGCTGTACTACACGCTCAAGAGAGCTGTGCGCCACCTGCGCCGAGAACCGCAAGTGA 300  
Db 314 ACGGCTGTACTACACGCTCAAGAGAGCTGTGCGCCACCTGCGCCGAGAACCGCA-GTGA 372

Qy 301 GCAAGTGTGAGATTCTCCAGACGATCATGACTACATCAGGAGACTTCATGTTGAGCTGA 360  
Db 373 GCAAGTGTGAGATTCTCCAGACGATCATGACTACATCAGGAGACTTCATGTTGAGCTGA 432  
Qy 361 ACTGGAAATCCGAAGTTGGAGCCCCCGGGGGCCGAGGGCTGCGGCTCCGCTCA 420  
Db 433 ACTGGAAATCCGAAGTTGGAGCCCCCGGGGGCCGAGGGCTGCGGCTCCGCTCA 492  
Qy 421 GCACCTTCAAGCGGAGATTCAGCGCTCTGACGCGCCGAGAGCGGCATGCTTCTTGAGAG 480  
Db 493 GCACCTTCAAGCGGAGATTCAGCGCTCTGACGCGCCGAGAGCGGCATGCTTCTTGAGAG 552  
Qy 481 ATCGCATTTGTGTGCTGAAAGCGCTCCCGCAGGAGACCGGCGAGCCCGACATCCAGG 540  
Db 553 ATCGCATTTGTGTGCTGAAAGCGCTCCCGCAGGAGACCGGCGAGCCCGACATCCAGG 612  
Qy 541 GGGCAAGAGAAATACGTGCTCTGTGGGTCTCCCGCAACGCGCTCGCGGATCTGAGGG 600  
Db 613 GGGCAAGAGAAATACGTGCTCTGTGGGTCTCCCGCAACGCGCTCGCGGATCTGAGGG 672  
Qy 601 AGAACAAGACCGATGGGGGCGGACCTGCGCCCTTAATCTGATCTCAGCTGGGGCTAGGCT 660  
Db 673 AGAACAAGACCGATGGGGGCGGACCTGCGCCCTTAATCTGATCTCAGCTGGGGCTAGGCT 732  
Qy 661 GAGGCACTGGGAGGAGGAGGGGCGCTCTCTGACACCTACTAGTCAACAGACTTTA 720  
Db 733 GAGGCACTGGGAGGAGGAGGGGCGCTCTCTGACACCTACTAGTCAACAGACTTTA 792  
Qy 721 GGGGGTGGGATTCACCTCGTGTGTTCTAATTTTGAAGAAGACATTTTAAAAATGG 780  
Db 793 GGGGGTGGGATTCACCTCGTGTGTTCTAATTTTGAAGAAGACATTTTAAAAATGG 852  
Qy 781 TCACGTTGGTGTCTCTGATGATTTCTGAGAAATGCTTTGATGTATATTAACATGAT 840  
Db 853 TCACGTTGGTGTCTCTGATGATTTCTGAGAAATGCTTTGATGTATATTAACATGAT 912  
Qy 841 CACCGACTGAGAAATGTTTGTACAAATGTTCTGTTGGGGCTGTTTTTGTATTAAACA 900  
Db 913 CACCGACTGAGAAATGTTTGTACAAATGTTCTGTTGGGGCTGTTTTTGTATTAAACA 972  
Qy 901 AATAATTTAGATGTGTAATAAAAAA 926  
Db 973 AATAATTTAGATGTGTAATAAAAAA 998

RESULT 7  
US-09-925-302-264  
; Sequence 264, Application US/09925302  
; Patent No. US20030064072A9  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA104  
; CURRENT APPLICATION NUMBER: US/09/925,302  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05918  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 896  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 264  
; LENGTH: 1027  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-302-264

Query Match 96.5%; Score 893.2; DB 10; Length 1027;  
Best Local Similarity 99.2%; Pred. No. 2,3e-249;  
Matches 919; Conservative 0; Mismatches 3; Indels 4; Gaps 2;  
Qy 4 GCCCATTCGTTTCAAGCCAGTCGCCAAGATCATGAAGTCCGACGTGGCAGACCGCA 63

Db 74 GCCCATCTGTTTACGCCAGTTCGCCAAGATCATGAAATGCGCAGTGGCAGACCGGCA 133  
Qy 64 CG 123  
Db 134 CG 193  
Qy 124 AGGTGTGCGGT 180  
Db 194 AGGTGTGCGGT 253  
Qy 181 GGGCG 240  
Db 254 GGGCG 313  
Qy 241 ACGGCTGTACTCAGCGCTCAGGAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300  
Db 314 ACGGCTGTACTCAGCGCTCAGGAGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 372  
Qy 301 GCAAGGTGAGATTTCTCCAGCAGTCACTACATCAGGAGACCTTCAGTTGAGCTGA 360  
Db 373 GCAAGGTGAGATTTCTCCAGCAGTCACTACATCAGGAGACCTTCAGTTGAGCTGA 432  
Qy 361 ACTGGGAATCCGGAATGGAGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420  
Db 433 ACTGGGAATCCGGAATGGAGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 492  
Qy 421 GCACCTCTCAACGCGGAGATCAGCGCGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480  
Db 493 GCACCTCTCAACGCGGAGATCAGCGCGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 552  
Qy 481 ATCGCATCTTGT 540  
Db 553 ATCGCATCTTGT 612  
Qy 541 GGGCGAAGGAATTAACGT 600  
Db 613 GGGCGAAGGAATTAACGT 672  
Qy 601 AGAACCAAGACCGATCG 660  
Db 673 AGAACCAAGACCGATCG 732  
Qy 661 GAGGCACTGCGGAGAGAGGCGCGCTCTCTGCACTAATGACAGCACTTTA 720  
Db 733 GAGGCACTGCGGAGAGAGGCGCGCTCTCTGCACTAATGACAGCACTTTA 792  
Qy 721 GGGGGTGGGATTTCCACTGT 780  
Db 793 GGGGGTGGGATTTCCACTGT 852  
Qy 781 TCACGTTGT 840  
Db 853 TCACGTTGT 912  
Qy 841 CACCGACTGAGAAATATGTTTACAAATGTTCTGTGGGCGTGTGTGTGTGTGTGTGTAA 900  
Db 913 CACCGACTGAGAAATATGTTTACAAATGTTCTGTGGGCGTGTGTGTGTGTGTGTGTAA 972  
Qy 901 AATAATTTAGT 926  
Db 973 AATAATTTAGT 998

RESULT 8  
US-10-384-339C-39  
Sequence 39, Application US/10384339C  
Publication No. US20040175703A1  
GENERAL INFORMATION:  
APPLICANT: Kreutzer, Roland  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GE  
FILE REFERENCE: 20200/2002  
CURRENT APPLICATION NUMBER: US/10/384,339C  
CURRENT FILING DATE: 2003-03-07

Qy PRIOR APPLICATION NUMBER: PCT/EP02/00152  
Db PRIOR FILING DATE: 2002-01-09  
Qy PRIOR APPLICATION NUMBER: DE 10100586.5  
Db PRIOR FILING DATE: 2001-01-09  
Qy PRIOR APPLICATION NUMBER: DE 10155280.7  
Db PRIOR FILING DATE: 2001-10-26  
Qy PRIOR APPLICATION NUMBER: DE 10158411.3  
Db PRIOR FILING DATE: 2001-11-29  
Qy PRIOR APPLICATION NUMBER: DE 10160151.4  
Db PRIOR FILING DATE: 2001-12-07  
Qy NUMBER OF SEQ ID NOS: 173  
Db SOFTWARE: PatentIn Ver. 2.1  
Qy SEQ ID NO 39  
Db LENGTH: 481  
Qy TYPE: DNA  
Db ORGANISM: Homo sapiens  
Qy PUBLICATION INFORMATION:  
Db TITLE: ID1  
Qy PATENT DOCUMENT NUMBER: X77956  
Db US-10-384-339C-39

Query Match 50.3%; Score 466; DB 17; Length 481;  
Best Local Similarity 100.0%; Pred. No. 4,7e-125;  
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 ATGAAAGTCCGAGTGGCAGACCGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 95  
Db 1 ATGAAAGTCCGAGTGGCAGACCGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60  
Qy 96 GCCCGCAAGACAGGAGCGGT 155  
Db 61 GCCCGCAAGACAGGAGCGGT 120  
Qy 156 GCATCTGT 215  
Db 121 GCATCTGT 180  
Qy 216 GTAAAGT 275  
Db 181 GTAAAGT 240  
Qy 276 ACCCTGCCAGAAACCGCAAGT 335  
Db 241 ACCCTGCCAGAAACCGCAAGT 300  
Qy 336 ATCAGGACCTTCAAGT 395  
Db 301 ATCAGGACCTTCAAGT 360  
Qy 396 GGGCTGCGGTTCGCGGCTCCGCTCAGCAACCTCAACGCGGAGATCAGCGCGCTGACGGCC 455  
Db 361 GGGCTGCGGTTCGCGGCTCCGCTCAGCAACCTCAACGCGGAGATCAGCGCGCTGACGGCC 420  
Qy 456 GAGCGGCGATGCTTCTGT 501  
Db 421 GAGCGGCGATGCTTCTGT 466

RESULT 9  
US-10-453-351-1  
Sequence 1, Application US/10453351  
Publication No. US2004001411A1  
GENERAL INFORMATION:  
APPLICANT: Young, Alison  
APPLICANT: Alan, Rhoda  
APPLICANT: Busam, Klaus  
TITLE OF INVENTION: Method for Evaluating a Tissue or Biopsy Sample to Determine if  
FILE REFERENCE: MSK P-056  
CURRENT APPLICATION NUMBER: US/10/453,351  
CURRENT FILING DATE: 2003-06-03  
PRIOR APPLICATION NUMBER: 60/386,298  
PRIOR FILING DATE: 2002-06-05



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; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 958
; TYPE: DNA
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: probe for Id1
US-10-453-351-1
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Query Match      47.9%; Score 443.6; DB 16; Length 958;
Beet Local Similarity 95.5%; Pred. No. 2,3e-118;
Matches 468; Conservative 0; Mismatches 19; Indels 3; Gaps 1;
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QY 4 GCCCATTTCTGTTTCAAGCCAGTCGCCAAGATATGAAAGTGGCCAGTGGCAGCACCGCCA 63
DB 31 GCCCATTTCTGTTTCAAGCCAGTCGCCAAGATATGAAAGTGGCCAGTGGCAGCACCGCCA 90
QY 64 CCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 123
DB 91 CCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 150
QY 124 AGGTGTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
DB 151 AGGTGTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 210
QY 181 GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
DB 211 GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 270
QY 241 ACGGCTGTACTCAAGCGCTCAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
DB 271 ACGGCTGTACTCAAGCGCTCAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 330
QY 301 GCAAGGTGAGATTTCTCCAGCAGTCATCTGATCATGAGGAGACCTTCAGTTGAGTGA 360
DB 331 GCAAGGTGAGATTTCTCCAGCAGTCATCTGATCATGAGGAGACCTTCAGTTGAGTGA 390
QY 361 ACTCGGAATCCGAAGTTGGAGACCCCGGGGGCGGAGGGGTGCGGGTCCGCTCA 420
DB 391 ACTCGGAATCCGAAGTTGGAGACCCCGGGGGCGGAGGGGTGCGGGTCCGCTCA 450
QY 421 GCACCTCAAGGGGAGATGAGCGGCGCTGAGCGGCGGAGGCGGAGCGGCTCTGCGGAG 480
DB 451 GCACCTCAAGGGGAGATGAGCGGCGCTGAGCGGCGGAGGCGGAGCGGCTCTGCGGAG 510
QY 481 ATCGCATCTT 490
DB 511 AGATCATCTCT 520
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RESULT 10
US-09-835-992A-30
; Sequence 30, Application US/09835992A
; Patent No. US20020037541A1
; GENERAL INFORMATION:
; APPLICANT: Obata, Yuichi
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED WITH GASTRIC CANCER AN
; FILE REFERENCE: L0461/7112
; CURRENT APPLICATION NUMBER: US/09/835,992A
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 08/896,164
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 30
; LENGTH: 721
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Unsure
; LOCATION: (264)..(264)
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; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: Unsure
; LOCATION: (488)..(488)
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: Unsure
; LOCATION: (512)..(512)
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: Unsure
; LOCATION: (538)..(538)
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: Unsure
; LOCATION: (548)..(548)
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: Unsure
; LOCATION: (605)..(605)
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: Unsure
; LOCATION: (611)..(611)
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: Unsure
; LOCATION: (660)..(660)
; OTHER INFORMATION: n = a, c, g or t
; NAME/KEY: Unsure
; LOCATION: (669)..(669)
; OTHER INFORMATION: n = a, c, g or t
US-09-835-992A-30
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Query Match      47.8%; Score 442.2; DB 9; Length 721;
Beet Local Similarity 95.1%; Pred. No. 5e-118;
Matches 466; Conservative 0; Mismatches 21; Indels 3; Gaps 1;
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QY 4 GCCCATTTCTGTTTCAAGCCAGTCGCCAAGATATGAAAGTGGCCAGTGGCAGCACCGCCA 63
DB 31 GCCCATTTCTGTTTCAAGCCAGTCGCCAAGATATGAAAGTGGCCAGTGGCAGCACCGCCA 90
QY 64 CCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 123
DB 91 CCGCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 150
QY 124 AGGTGTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
DB 151 AGGTGTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 210
QY 181 GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
DB 211 GGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 270
QY 241 ACGGCTGTACTCAAGCGCTCAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
DB 271 ACGGCTGTACTCAAGCGCTCAAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 330
QY 301 GCAAGGTGAGATTTCTCCAGCAGTCATCTGATCATGAGGAGACCTTCAGTTGAGTGA 360
DB 331 GCAAGGTGAGATTTCTCCAGCAGTCATCTGATCATGAGGAGACCTTCAGTTGAGTGA 390
QY 361 ACTCGGAATCCGAAGTTGGAGACCCCGGGGGCGGAGGGGTGCGGGTCCGCTCA 420
DB 391 ACTCGGAATCCGAAGTTGGAGACCCCGGGGGCGGAGGGGTGCGGGTCCGCTCA 450
QY 421 GCACCTCAAGGGGAGATGAGCGGCGCTGAGCGGCGGAGGCGGAGCGGCTCTGCGGAG 480
DB 451 GCACCTCAAGGGGAGATGAGCGGCGCTGAGCGGCGGAGGCGGAGCGGCTCTGCGGAG 510
QY 481 ATCGCATCTT 490
DB 511 AMATCATCTCT 520
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RESULT 11
US-10-027-632-141641
; Sequence 141641, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
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/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ TITLE OF INVENTION: Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.129
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 141641
/ LENGTH: 663
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-141641

Query Match      39.4%; Score 364.8; DB 13; Length 663;
Best Local Similarity 94.6%; Pred. No. 1.7e-95;
Matches 388; Conservative 1; Mismatches 18; Indels 3; Gaps 1;

QY      84 TGGCGCTGAAGCGCGGCAAGACAGCGAGCGGTGCGGCGAGTGTGCTGTCT 143
DB      1 TGGCGCTGAAGCGCGGCAAGACAGCGAGCGGTGCGGCGAGTGTGCTGTCT 60
QY     144 GAGCAGAGCGTGGCCATCTCGCGCTG---CCGGGGGCGCGGGCGCGCTGCTG 200
DB      61 GAGCAGAGCGTGGCCATCTCGCGCTGCGCGGGGCGCGGGCGCGCTGCTG 120
QY     201 CTGACGAGCAGAGGTAAGTGTGCTCTACGACATGAAAGCGTGTATCTACGCTC 260
DB     121 CTGACGAGCAGAGGTAAGTGTGCTCTACGACATGAAAGCGTGTATCTACGCTC 180
QY     261 AAGGAGCTGTGCCACCTGCCCGAAGCCGCAAGGTGAGCAAGTGTGAGATTCTCAG 320
DB     181 AAGGAGCTGTGCCACCTGCCCGAAGCCGCAAGGTGAGCAAGTGTGAGATTCTCAG 240
QY     321 CACGTATGACTATCATCACTAGGAGACCTTCAAGTGTGAACTGAACTCGAATCGAATTGG 380
DB     241 CACGTATGACTATCATCACTAGGAGACCTTCAAGTGTGAACTGAACTCGAATCGAATTGG 300
QY     381 ACCCGCGGGGCGGAGGCTGCGGCTCGGGCTCGGCTCGAGCAACCTCAACGGGAGATC 440
DB     301 ACCCGCGGGGCGGAGGCTGCGGCTCGGGCTCGGCTCGAGCAACCTCAACGGGAGATC 360
QY     441 AGCGCCCTGACGCGCGGAGGCGGATGCGTTCTCTGCGAGCATCGCATCTT 490
DB     361 AGCGCCCTGACGCGCGGAGGCGGATGCGATTCGACCATGATCATCTCT 410

RESULT 12
US-10-027-632-141641
/ Sequence 141641, Application US/10027632
/ Publication No. US20030204075A9
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
/ TITLE OF INVENTION: Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.129
/ CURRENT APPLICATION NUMBER: US/10/027,632
/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
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/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 141641
/ LENGTH: 663
/ TYPE: DNA
/ ORGANISM: Human
US-10-027-632-141641

Query Match      39.4%; Score 364.8; DB 15; Length 663;
Best Local Similarity 94.6%; Pred. No. 1.7e-95;
Matches 388; Conservative 1; Mismatches 18; Indels 3; Gaps 1;

QY      84 TGGCGCTGAAGCGCGGCAAGACAGCGAGCGGTGCGGCGAGTGTGCTGTCT 143
DB      1 TGGCGCTGAAGCGCGGCAAGACAGCGAGCGGTGCGGCGAGTGTGCTGTCT 60
QY     144 GAGCAGAGCGTGGCCATCTCGCGCTG---CCGGGGGCGCGGGCGCGCTGCTG 200
DB      61 GAGCAGAGCGTGGCCATCTCGCGCTGCGCGGGGCGCGGGCGCGCTGCTG 120
QY     201 CTGACGAGCAGAGGTAAGTGTGCTCTACGACATGAAAGCGTGTATCTACGCTC 260
DB     121 CTGACGAGCAGAGGTAAGTGTGCTCTACGACATGAAAGCGTGTATCTACGCTC 180
QY     261 AAGGAGCTGTGCCACCTGCCCGAAGCCGCAAGGTGAGCAAGTGTGAGATTCTCAG 320
DB     181 AAGGAGCTGTGCCACCTGCCCGAAGCCGCAAGGTGAGCAAGTGTGAGATTCTCAG 240
QY     321 CACGTATGACTATCATCACTAGGAGACCTTCAAGTGTGAACTGAACTCGAATCGAATTGG 380
DB     241 CACGTATGACTATCATCACTAGGAGACCTTCAAGTGTGAACTGAACTCGAATCGAATTGG 300
QY     381 ACCCGCGGGGCGGAGGCTGCGGCTCGGGCTCGGCTCGAGCAACCTCAACGGGAGATC 440
DB     301 ACCCGCGGGGCGGAGGCTGCGGCTCGGGCTCGGCTCGAGCAACCTCAACGGGAGATC 360
QY     441 AGCGCCCTGACGCGCGGAGGCGGATGCGTTCTCTGCGAGCATCGCATCTT 490
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US-10-291-172-420
/ Sequence 420, Application US/10291172
/ Publication No. US20030228584A1
/ GENERAL INFORMATION:
/ APPLICANT: HySeq, Inc
/ TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
/ FILE REFERENCE: 21272-045
/ CURRENT APPLICATION NUMBER: US/10/291,172
/ CURRENT FILING DATE: 2000-11-08
/ PRIOR APPLICATION NUMBER: 09/693,267
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 09/665,363
/ PRIOR FILING DATE: 2000-09-19
/ PRIOR APPLICATION NUMBER: 09/616,847
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: 09/596,193
/ PRIOR FILING DATE: 2000-06-17
/ PRIOR APPLICATION NUMBER: 09/574,454
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;; PRIOR FILING DATE: 2000-05-19  
;; PRIOR APPLICATION NUMBER: 09/519,705  
;; PRIOR FILING DATE: 2000-03-07  
;; NUMBER OF SEQ ID NOS: 752  
;; SEQ ID NO: 420  
;; LENGTH: 1049  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-10-291-172-420

Query Match 37.1%; Score 343.4; DB 15; Length 1049;  
Best Local Similarity 74.7%; Pred. No. 3.7e-89;  
Matches 742; Conservative 0; Mismatches 181; Indels 70; Gaps 22;

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DB 55 GCCCATTTCTGTTTCCAGTGTGCGCAAGAAATCATGAAGTCCCGCATGGCAGCACCGGCA 114
QY 64 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 122
DB 115 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 174
QY 123 GAGGTGTGCGCTGTCTGT-CTGAGCAGACGCTGCGCAT-----CTGCGCTGCGCGG 175
DB 175 GAGGTGTGCGCTGTCTGTACTGACAGAGCGTGGCAATTCTCGCGTTGCCCGCGGCGG 234
QY 176 CGCGCGCGCGCGCGCTGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 233
DB 235 CGCGCGCGCGCGCGCTGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 294
QY 234 GACA-TGAACGGCTGTT-ACTCAGCGCTCAAGAGCTGGTCCCAACCTGCGCC-----AG 287
DB 295 GACATTGAACGGCTGTTAATCAACGCTCAAGAGAGCTGGTCCCAACCTGCGCCCAAGAA 354
QY 288 AACCGCAAGGTGAGCAAGGTGAGATTCTCCAGCAGCTCATC-----GACTACATC 338
DB 355 CCGCGCAAGGTGAGCAAGGTGAGATTCTCCAGCAGCTCATC-----GACTACATCAG 414
QY 339 AGGAACTTCAAGTTGAGAGTGA---CTCGAATTCGAAAGTTGGGACCCCGCGGCGCG 394
DB 415 GAACTTTCAGTTGGAGAGCTGAACCTTCGCGAATCCCGAAGTTGGGAAACCCCGCGGCG 474
QY 395 AGGCTGCGCGGTCCGCGGCTCCGCTC-----AGCAACCTCAACGCGGAGAT--CAGCGC 446
DB 475 CGAGGCGCTCGCGGCTCCGCGGCTCCGCTCAAGCAACCTCAACGCGGAGATTCAGCGCC 534
QY 447 CTGACGCGCGAG--CGGATCGTTCCTGCGGAGATGCACTTGTGTCTGCTGAAGCG 504
DB 535 CTGACGCGCGAGGCGGCGCATGCGTTCTGCGGAGATGCACTTGTGTCTGCTGAAGCG 594
QY 505 CCTCCCCAGGAGACCGGCGGACCCCAACCATCA-----GGGCGCAAGGAAATTAC 556
DB 595 CCTTCCCCAGGAGACCGGCGGAGACCCCAACCATCA-----GGGCGCGGAGAAATTAC 654
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QY 665 CACTGCGAGAGAGAGGCGCTCTCTCTGAC--ACTTACTAGTCAACAGACTTTAAG 722
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QY 723 GGGTGGGAAAT--CCACTGCTGTGTTCTAATTTTT--GAAACAGACATTTTAAAAATG 779
DB 835 GGGTGGGAAATCCCACTGCTGTGTTCTAATTTTTTTTGAAGAGAGACATTTTAAATG 894
QY 780 GTCAAGTTGTGTCTTCTAGATTTCTAGAGAAATTC--TTTGTATGTATATTACAT 837
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RESULT 14  
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Sequence 420, Application US/10221278  
Publication No. US20040034208A1  
GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: No. US20040034208A1 Nucleic Acids and Polypeptides  
; FILE REFERENCE: 21272-045  
; CURRENT APPLICATION NUMBER: US/10/221,278  
; PRIOR FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: 09/693,267  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 09/665,363  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 09/616,847  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: 09/596,193  
; PRIOR FILING DATE: 2000-06-17  
; PRIOR APPLICATION NUMBER: 09/574,454  
; PRIOR FILING DATE: 2000-05-19  
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; NUMBER OF SEQ ID NOS: 752  
; SEQ ID NO: 420  
; LENGTH: 1049  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-221-278-420

Query Match 37.1%; Score 343.4; DB 16; Length 1049;  
Best Local Similarity 74.7%; Pred. No. 3.7e-89;  
Matches 742; Conservative 0; Mismatches 181; Indels 70; Gaps 22;

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QY 4 GCCCATTTCTGTTTCCAGTGTGCGCAAGAAATCATGAAGTCCCGCATGGCAGCACCGGCA 63
DB 55 GCCCATTTCTGTTTCCAGTGTGCGCAAGAAATCATGAAGTCCCGCATGGCAGCACCGGCA 114
QY 64 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 122
DB 115 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 174
QY 123 GAGGTGTGCGCTGTCTGT-CTGAGCAGACGCTGCGCAT-----CTGCGCTGCGCGG 175
DB 175 GAGGTGTGCGCTGTCTGTACTGAGCAGAGGTGGCATTTCTCGCGTTGCCCGCGGCGG 234
QY 176 CGCGGCGCGCGCTGCTGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 233
DB 235 CGCGGCGCGCGCTGCTGCTGCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 294
QY 234 GACA-TGAACGGCTGTT-ACTCAGCGCTCAAGAGCTGGTCCCAACCTGCGCC-----AG 287
DB 295 GACATTGAACGGCTGTTAATCAACGCTCAAGAGAGCTGGTCCCAACCTGCGCCCAAGAA 354
QY 288 AACCGCAAGGTGAGCAAGGTGAGATTCTCCAGCAGCTCATC-----GACTACATC 338
DB 355 CCGCGCAAGGTGAGCAAGGTGAGATTCTCCAGCAGCTCATC-----GACTACATTCAG 414
QY 339 AGGAACTTCAAGTTGAGAGTGA---CTCGAATTCGAAAGTTGGGACCCCGCGGCGCG 394
DB 415 GAACTTTCAGTTGGAGAGCTGAACCTTCGGAATTCGGAATTCGGAACCCCGCGGCGCG 474
QY 395 AGGCTGCGCGGTCCGCGGCTCCGCTC-----AGCAACCTCAACGCGGAGAT--CAGCGC 446
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Db 1015 TTAACAATAATTTAGATGTAAGAAAAA 1047

RESULT 15  
US-09-835-992A-31/c  
; Sequence 31, Application US/09835992A  
; Patent No. US2002037541A1  
; GENERAL INFORMATION:  
; APPLICANT: Obata, Yuichi  
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED WITH GASTRIC CANCER AN  
; FILE REFERENCE: L0461/7112  
; CURRENT APPLICATION NUMBER: US/09/835,992A  
; PRIORITY FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: US 08/896,164  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 31  
; LENGTH: 461  
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; ORGANISM: Homo sapiens  
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/ US-09-835-992A-31
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Best Local Similarity 79.3%; Pred. No. 8.1e-89;
Matches 365; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

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    |||||
QY 517 ACCGCGGACCCCGACCCATCCAGCGGCGGAGAGAAATTAATGCTCTGTCGCTCTCC 576
    |||||
DB 401 ACCGCGGACCCCGACCCATCCAGCGGCGGAGAGAAATTAATGTTGTTGCTTCC 342
    |||||
QY 577 AACGCGCTCGCGCGATTCGAGGAGAAACAAGACCGGCGGCGGCTGAGCCCTTAAC 636
    |||||
DB 341 NAAGNGCCTTGCCGGAATTTGNGGAGNAGNAGNCCGATTCGCGCAATGNGCCCTTAA 282
    |||||
QY 637 TGCATCCAGCCTGCGGCTGAGGCTGAGGCACTGCGAGAGAGAGGCGCTCTCTGAC 696
    |||||
DB 281 TGNATNCAGCCTGCGGNTGNGAGTGAAGCAATGNGAGAGGNGGTTCTTTTGNAN 222
    |||||
QY 697 ACCTACTAGTACCAAGACCTTAAGGGGTGGATTCACCTCGTGTGTTCTATTTTGG 756
    |||||
DB 221 ACCTAATAGTNACCAAGAAATTAAGGGGTGGANTNCAATGNGGTTTATTTTGG 162
    |||||
QY 757 AAAAGCAGACATTTTAAAAAATGTCACGTTTGTCTTCAATTTCTAGAGAAATG 816
    |||||
DB 161 NAAAGCAGAAATTTTAAAAAATGTTAGTTGTTTNAAGATTTTNGGAANTG 102
    |||||
QY 817 CTTGTATTTATATATTAATGATCAACGACCTGAGAAATATGTTTACATAGTTCTGTG 876
    |||||
DB 101 NTTGTATTTGTAATATACNANGATNACCGAATGAAAATATGTTTACNATAGTTGTG 42
    |||||
QY 877 GGGCTGTTTTTTGTTTAAACAATTAATTTAGATG 916
    |||||
DB 41 GGGNTGTTTTTTGTTTAAANNAATTAATTAAGTGTG 2
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Job time : 549.117 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2004, 15:00:58 ; Search time 3370.83 Seconds  
(without alignments)  
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Title: US-09-996-529A-4

Perfect score: 926  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hic: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gse1: \*  
9: gb\_gse2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	897	96.9	950	3	CR591965 full-length
2	897	96.9	952	3	CR615862 full-length
3	897	96.9	970	3	CR599901 full-length
4	895.2	96.7	958	3	CR621997 full-length
5	887.4	95.8	951	1	AL546878 full-length
6	866.2	93.5	939	3	CR600217 full-length
7	844.4	91.2	938	5	BX37234 full-length
8	844	91.1	868	3	CR610338 full-length
9	841.4	90.9	1002	4	BM919830 full-length
10	828	88.6	1059	4	BM544445 full-length
11	820.8	88.6	870	5	BX380789 full-length
12	820.2	88.6	1081	4	BM918524 full-length
13	814.8	88.0	934	4	AL576138 full-length
14	813.4	87.8	839	6	CA777979 full-length
15	813.2	87.8	961	1	AL553031 full-length
16	794.6	85.8	996	4	BM559163 full-length
17	793.8	85.7	855	4	CR593062 full-length
18	793.2	85.7	1061	4	BM609372 full-length
19	781.8	84.4	886	4	AL546843 full-length
20	777.8	84.0	1021	4	BM556765 full-length
21	767.8	82.9	856	5	BX373593 full-length
22	758	81.9	830	2	BF568977 full-length
23	758	81.9	836	1	AL525027 full-length
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25	752.2	81.2	897	4	BG682892	BG682892	602651087
26	750.4	81.0	1128	4	BM541894	BM541894	170006001
27	748.8	80.9	762	7	CR264895	CR264895	190006001
28	738.6	79.8	865	5	BX437235	BX437235	602651087
29	737.2	79.6	994	5	BQ219146	BQ219146	601494082
30	736.6	79.5	1129	2	BE621829	BE621829	170005999
31	734.2	79.3	794	7	CR264925	CR264925	601304627
32	733.8	79.2	854	4	B1819212	B1819212	601304627
33	732.8	79.1	939	5	BQ926660	BQ926660	AGENCOURT
34	729.2	78.7	1083	5	BQ277663	BQ277663	AGENCOURT
35	727.2	78.5	882	5	BQ222774	BQ222774	AGENCOURT
36	719.4	77.7	921	5	BX395514	BX395514	AGENCOURT
37	719.2	77.7	732	5	BQ625137	BQ625137	UI-H-FG1
38	718.6	77.6	811	1	A1346430	A1346430	QPS0608
39	718	77.5	886	5	BQ229885	BQ229885	AGENCOURT
40	717.2	77.5	730	5	BM977684	BM977684	UI-CF-EV1
41	716.4	77.4	807	4	B1255137	B1255137	602975992
42	716.2	77.3	856	5	BQ433990	BQ433990	AGENCOURT
43	716.2	77.3	886	5	B177698	B177698	AGENCOURT
44	714	77.1	732	7	CM479126	CM479126	UI-CF-FN0
45	713.6	77.1	840	5	BQ940719	BQ940719	AGENCOURT

#### ALIGNMENTS

RESULT 1	CR591965	950 bp	mrna	linear	HTC 21-JUL-2004
LOCUS	CR591965	full-length cDNA clone	CSOD1049YN03	of Placenta Cot	25-normalized
DEFINITION	CR591965	full-length cDNA clone	CSOD1049YN03	of Homo sapiens	(human).
ACCESSION	CR591965	1	GI:50472772		
VERSION	CR591965.1				
KEYWORDS	HTC; CNSLT_CDNA.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Li, W.B., Graber, C., Jeesee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 950)				
REFERENCE	Genoscope.				
AUTHORS	Direct Submission				
TITLE	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage ;				
JOURNAL	BP 191 91006 EVRY cedex - FRANCE (E-mail: sequef@genoscope.cns.fr				
COMMENT	- Web : www.genoscope.cns.fr) 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime				
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library				
	was normalized. Library was constructed by Life Technologies, a				
	division of Invitrogen.				
FEATURES	Location/Qualifiers				
source	1..950				
	/organism="Homo sapiens"				
	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="CSOD1049YN03"				
	/tissue_type="Placenta Cot 25-normalized"				
	/plasmid="pCMVSPORT_6"				
ORIGIN					
Query Match	96.9%; Score 897; DB 3; Length 950;				
Best local Similarity	99.1%; Pred.No.2.5e-21;				
Matches	913; Conservative 0; Mismatches 5; Indels 3; Gaps 1;				
OY	4	GGCCATTCGTTGAGCCAGTCGCCAGATCAATGAAGTGCAGCCAGACACCGCA	63		
DB	30	GCCATTCTGTTTTCAGCCAGTCGCCAGATCAATGAAGTGCAGCCAGACACCGCA	89		

QY	64	CCGCCGCCGCCGCCCGCCCGCTGAAAGCCCGGACAGACAGCAGCGGTGCGGACG	123
Db	90	CCGCCGCCGCCGCCCGCCCGCTGAAAGCCCGGACAGACAGCAGCGGTGCGGACG	149
QY	124	AGGTGAGTCCGTGCTGTGTCGAGAGACCGTGGCATCTTGCGCGTG--CCGCGGCCCG	180
Db	150	AGGTGAGTCCGTGCTGTGTCGAGAGACCGTGGCATCTTGCGCGTGGCGCGGCCCG	209
QY	181	GGGCGCGCTGCGCTGCGCTGCGAGCAGACAGCAGTAAACGTGCTCTCTACGACATGA	240
Db	210	GGGCGCGCTGCGCTGCGCTGCGAGCAGACAGTAAACGTGCTCTCTACGACATGA	269
QY	241	ACGCGTGTCTCAACGCGCTCAAGAGAGCTGTGGCCACCTCGGCCAAGACCGAAGTGA	300
Db	270	ACGCGTGTCTCAACGCGCTCAAGAGAGCTGTGGCCACCTCGGCCAAGACCGAAGTGA	329
QY	301	GCAAGGTGAGATCTTCCAGCAGCTCATCACTACAGGAGCCTTCAAGTTGAGACTGA	360
Db	330	GCAAGGTGAGATCTTCCAGCAGCTCATCACTACAGGAGCCTTCAAGTTGAGACTGA	389
QY	361	ACTCGGAATCCGAAGTTGGGACCCCGCGGGGCCGAGGGCTGCGCGGTCCGCTCA	420
Db	390	ACTCGGAATCCGAAGTTGGGACCCCGCGGGGCCGAGGGCTGCGCGGTCCGCGCTCA	449
QY	421	GCACCCTCAACGCGCAGATCAGGCGCCTGACGCGCGAGCGGACATGCCGTTCTCGGAGAC	480
Db	450	GCACCCTCAACGCGCAGATCAGGCGCCTGACGCGCGAGCGGACATGCCGTTCTCGGAGAC	509
QY	481	ATTCGATCTTTGTGTGCTGAGAGCGCTCCCGAAGGACCGGCGGACCCGACGATCCAGG	540
Db	510	ATTCGATCTTTGTGTGCTGAGAGCGCTCCCGAAGGACCGGCGGACCCGACGATCCAGG	569
QY	541	GGGCAAGAGGAATTACGTGCTCTGAGGGGTCTCCCCAAGCGCCCTGCGCGAATCTGAGGG	600
Db	570	GGGCAAGAGGAATTACGTGCTCTGAGGGGTCTCCCCAAGCGCCCTGCGCGAATCTGAGGG	629
QY	601	AGAACAGACCGATCGCGCGGCCACTGCGGCTTAACTGCATCAGCCTGCGGCTGAGGCT	660
Db	630	AGAACAGACCGATCGCGCGGCCACTGCGGCTTAACTGCATCAGCCTGCGGCTGAGGCT	689
QY	661	GAGGCACTGCGCAGAGAGAGGGGCGTCCCTCTGCGCACACTTACGTACCAAGACTTTA	720
Db	690	GAGGCACTGCGCAGAGAGAGGGGCGTCCCTCTGCGCACACTTACGTACCAAGACTTTA	749
QY	721	GGGGGTGAGATTCACCTGCTGTGTTCTAATTTTTGAAACAGACATTTAAAAAAATGG	780
Db	750	GGGGGTGAGATTCACCTGCTGTGTTCTAATTTTTGAAACAGACATTTAAAAAAATGG	809
QY	781	TCAGCTTGTGTGCTTCTCAGATTTCTGAGAAATTTGCTTTGTATGTATTAACAATGAT	840
Db	810	TCAGCTTGTGTGCTTCTCAGATTTCTGAGAAATTTGCTTTGTATGTATTAACAATGAT	869
QY	841	CACCGACTGAGAAATATGTTTTTAACAATAGTCTGAGGGGCGTTTTTTGTATTAACA	900
Db	870	CACCGACTGAGAAATATGTTTTTAACAATAGTCTGAGGGGCGTTTTTTGTATTAACA	929
QY	901	AATAATTTAGTGTGAAAAA 921	
Db	930	AATAATTTAGTGTGAAAAA 950	

RESULT 2	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
CR615862	CR615862	full-length cDNA clone CS0D1026YX10 of Placenta Cot 25-normalized	CR615862	CR615862.1	GI:50496669	HTC; CNSLT_cDNA. Homo sapiens (human)	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	AUTHORS	TITLE	JOURNAL	REMARK
REFERENCE	AUTHORS	TITLE <td>JOURNAL</td> <td>REMARK</td>	JOURNAL	REMARK
1	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.	Full-length cDNA libraries and normalization	Unpublished	
2	Farady Avenue	BP 191 91006 EXRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)		
3	Genoscope.	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage		
4	Genoscope.	BP 191 91006 EXRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)		
5	Genoscope.	Web : www.genoscope.cns.fr		
6	Genoscope.	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prim		
7	Genoscope.	end enriched, double-strand cDNA was digested with Not I and clone		
8	Genoscope.	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library		
9	Genoscope.	was normalized. Library was constructed by Life Technologies, a		
10	Genoscope.	division of Invitrogen.		
11	Genoscope.	Location/Qualifiers		
12	Genoscope.	1.952		
13	Genoscope.	/organism="Homo sapiens"		
14	Genoscope.	/mol_type="mrna"		
15	Genoscope.	/db_xref="taxon:9606"		
16	Genoscope.	/clone="CSODI026YK10"		
17	Genoscope.	/issue_type="Placenta Cot 25-normalized"		
18	Genoscope.	/plasmid="pCMVSPORT_6"		
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100	Genoscope.			



QY 601 AGAACAAGACCGATCGGCGGCACCTGCGCCTTAACTGCATCCAGCTGGGCTGAGCT 660  
DB 632 AGAACAAGACCGATCGGCGGCACCTGCGCCTTAACTGCATCCAGCTGGGCTGAGCT 691  
QY 661 GAGGCACTGGCGAGAGAGAGGCGCTCTCTCTGCAACACCTACTAGTCAACAGAGACTTTA 720  
DB 692 GAGGCACTGGCGAGAGAGAGGCGCTCTCTCTGCAACACCTACTAGTCAACAGAGACTTTA 751  
QY 721 GGGGGTGGGATTCCTGCTGTGTTCTATTTTGGAAAAGAGACATTTTAAATAATG 780  
DB 752 GGGGGTGGGATTCCTGCTGTGTTCTATTTTGGAAAAGAGACATTTTAAATAATG 811  
QY 781 TCACGTTGGTCTCTCAGATTTCTGAGGAATGCTTTGATTTATTTACATGAT 840  
DB 812 TCACGTTGGTCTCTCAGATTTCTGAGGAATGCTTTGATTTATTTACATGAT 871  
QY 841 CACGCACTGAGAAATTTGTTTACAAATGTTGTGGGGCTGTTTTTGTATTAAACA 900  
DB 872 CACGCACTGAGAAATTTGTTTACAAATGTTGTGGGGCTGTTTTTGTATTAAACA 931  
QY 901 AATAATTAGATGTGTAATAA 921  
DB 932 AATAATTAGATGTGTAATAA 952

## RESULT 3

LOCUS CR599901 970 bp mRNA linear HTC 21-JUL-2004  
DEFINITION full-length cDNA clone CSOD1072Y105 of Placenta Cot 25-normalized  
of Homo sapiens (human).

ACCESSION CR599901  
VERSION CR599901.1 GI:50480708  
KEYWORDS HTC; CNSLT\_cDNA.

SOURCE Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 970)  
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

Full-length cDNA libraries and normalization  
Unpublished

Contact : Feng Liang Email : fliang@life.techn.com URL :  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Paradey Avenue

2 (bases 1 to 970)

Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr

- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.

Location/Qualifiers

1..970

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CSOD1072Y105"

/issue\_type="Placenta Cot 25-normalized"

/plasmid="pCMVSPORT\_6"

## ORIGIN

Query Match 96.9%; Score 897; DB 3; Length 970;  
Best Local Similarity 99.1%; Pred. No. 2.5e-211;

Matches 913; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

QY 4 GCCCATCTGTTTCAGCGAGTGGCCAAAGATCATGAAAGTCCGACGTGCGACACCGCA 63  
DB 50 GCCCATCTGTTTCAGCGAGTGGCCAAAGATCATGAAAGTCCGACGTGCGACACCGCA 109

QY 64 CCGCCCGCGGCGCCCAAGCTGCGGCTGAAAGCGCGCAAGACAGCGGTGCGGCG 123  
DB 110 CCGCCCGCGGCGCCCAAGCTGCGGCTGAAAGCGCGCAAGACAGCGGTGCGGCG 169  
QY 124 AGGTGTCGCTGTCTGTCTGTAGCAGACGTGCGCATCTCGGCTG--CGGGGCGCG 180  
DB 170 AGGTGTCGCTGTCTGTCTGTAGCAGACGTGCGCATCTCGGCTGCGGCGCGGCG 229  
QY 181 GGGCGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 240  
DB 220 GGGCGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 289  
QY 241 ACGGCTGTTTACTCAGCGCTCAAGAGCTGAGTCCGACCTGCGGCGCAAGACCGCAAGTGA 300  
DB 280 ACGGCTGTTTACTCAGCGCTCAAGAGCTGAGTCCGACCTGCGGCGCAAGACCGCAAGTGA 349  
QY 301 GCAGGTGAGATTTCTGAGCAGCGATCATGATCATGAGGACCTTCAAGTGAAGCTGA 360  
DB 350 GCAGGTGAGATTTCTGAGCAGCGATCATGATCATGAGGACCTTCAAGTGAAGCTGA 409  
QY 361 ACTCGGAATCCGAAATTTGAGAACCCCGGGGGCGGAGGCTGCGGCTCGGCTCA 420  
DB 410 ACTCGGAATCCGAAATTTGAGAACCCCGGGGGCGGAGGCTGCGGCTCGGCTCA 469  
QY 421 GCACCTCAAGCGGCGAGATCAGCGGCTGAGCGGCGGCGGCGGCGGCGGCGGCGG 480  
DB 470 GCACCTCAAGCGGCGAGATCAGCGGCTGAGCGGCGGCGGCGGCGGCGGCGGCGG 529  
QY 481 ATGCGATCTTGTGTGCTGAGAGCGGCTCCCGAGGAGCGGCGGAGCCCGAGCATTCAGG 540  
DB 530 ATGCGATCTTGTGTGCTGAGAGCGGCTCCCGAGGAGCGGCGGAGCCCGAGCATTCAGG 589  
QY 541 GGGCAAGAGAAATTCGTCGCTGTGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 600  
DB 590 GGGCAAGAGAAATTCGTCGCTGTGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 649  
QY 601 AGAACAAGACCGATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 660  
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QY 710 GAGGCACTGGCGAGAGAGAGGCGGCTCTCTGCAACCTACTAGTCAACAGACTTTA 769  
DB 721 GGGGCTGGGATTCACCTGCTGTGTTTCTAATTTTGAAGAGACATTTTAAATAATG 780  
QY 770 GGGGCTGGGATTCACCTGCTGTGTTTCTAATTTTGAAGAGACATTTTAAATAATG 829  
DB 781 TCACGTTGGTCTCTCAGATTTCTGAGGAATGCTTGTATTTATTTACATGAT 840  
QY 830 TCACGTTGGTCTCTCAGATTTCTGAGGAATGCTTGTATTTATTTACATGAT 889  
DB 841 CACGCACTGAGAAATTTGTTTACAAATGTTCTGTGGGCTGTTTTTGTATTAAACA 900  
QY 890 CACGCACTGAGAAATTTGTTTACAAATGTTCTGTGGGCTGTTTTTGTATTAAACA 949  
DB 901 AATAATTAGATGTGTAATAA 921  
DB 950 AATAATTAGATGTGTAATAA 970

## RESULT 4

LOCUS CR621997

DEFINITION full-length cDNA clone CSODJ014YE10 of T cells (Jurkat cell line)

Full 10-normalized of Homo sapiens (human).

ACCESSION CR621997

VERSION CR621997.1 GI:50502804

KEYWORDS HTC; CNSLT\_cDNA.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
1 (bases 1 to 958)  
AUTHORS  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE  
Full-length cDNA libraries and normalization  
JOURNAL  
Unpublished  
REMARK  
Contact: Feng Liang Email: fliang@lifetech.com URL:  
http://fulllength.invitrogen.com/Invitrogen Corporation 1600  
Faraday Avenue  
2 (bases 1 to 958)  
REFERENCE  
AUTHORS  
JOURNAL  
Genoscope.  
Direct Submission  
Submitted (20-UTR-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
Location/Qualifiers  
1. 958  
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10-normalized"  
/plasmid="pCMVSPORT\_6"

COMMENT  
FEATURES  
Source  
Location/Qualifiers  
1. 958  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0D1014E10"  
/tissue\_type="T cells (Jurkat cell line) Cot  
10-normalized"  
/plasmid="pCMVSPORT\_6"

## ORIGIN

Query Match 96.7%; Score 895.2; DB 3; Length 958;  
Best Local Similarity 99.3%; Pred. No. 7e-211;  
Matches 910; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 4 GCCCATTTCTGTTTACGACGATCGCCAAAGATCATGAATTCGCGAGTGCACACCGCCA 63  
DB 43 GCCCATTTCTGTTTACGACGATCGCCAAAGATCATGAATTCGCGAGTGCACACCGCCA 102  
QY 64 CCG 123  
DB 103 CCG 162  
QY 124 AGGTGTGCGCTGTCTGTCTGTGACAGAGCGTGGCCATCTCGGCGG---CCGCGCGCGCG 180  
DB 163 AGGTGTGCGCTGTCTGTCTGTGACAGAGCGTGGCCATCTCGGCGGCGCGCGCGCGCG 222  
QY 181 GGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240  
DB 223 GGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 282  
QY 241 ACAGCTGTACTCAGCGCTCAGAGAGCGTGGTGGCCACCTGCGCGCGCGCGCGCGCGCG 300  
DB 283 ACAGCTGTACTCAGCGCTCAGAGAGCGTGGTGGCCACCTGCGCGCGCGCGCGCGCGCG 342  
QY 301 GCAAGGTGAGATTTCTCAGACGTCATCATCATCATCATCATCATCATCATCATCATCAT 360  
DB 343 GCAAGGTGAGATTTCTCAGACGTCATCATCATCATCATCATCATCATCATCATCATCAT 402  
QY 361 ACTGGGAATTCGAATTTGGAGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCA 420  
DB 403 ACTGGGAATTCGAATTTGGAGACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCA 462  
QY 421 GCACCTCTCAGCG 480  
DB 463 GCACCTCTCAGCG 522  
QY 481 ATTCGATTTGT 540  
DB 523 ATTCGATTTGT 582  
QY 541 GGGCGAAGAGAAATTAAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600  
DB 583 GGGCGAAGAGAAATTAAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 642

QY 601 AGAACAAGACCGATCGCT 660  
DB 643 AGAACAAGACCGATCGCT 702  
QY 661 GAGGACACTGCGGAGAGAGAGCGCGCTCTCTGTGACACTTACTAGTACACGAGACTTTA 720  
DB 703 GAGGACACTGCGGAGAGAGAGCGCGCTCTCTGTGACACTTACTAGTACACGAGACTTTA 762  
QY 721 GGGGCTGGGATTTCCACTGT 780  
DB 763 GGGGCTGGGATTTCCACTGT 822  
QY 781 TCACGTTTGTGCTTCTTCTGAGAAATTTGTTGATTTGATTTGATTTGATTTGATTTGAT 840  
DB 823 TCACGTTTGTGCTTCTTCTGAGAAATTTGTTGATTTGATTTGATTTGATTTGATTTGAT 882  
QY 841 CACGACCTGAGAAATTTGTTTACATATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900  
DB 883 CACGACCTGAGAAATTTGTTTACATATGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 942  
QY 901 AATAATTTAGATGGTG 916  
DB 943 AATAATTTAGATGGTG 958

RESULT 5  
AL546878 951 bp mRNA linear EST 25-MAR-2004  
LOCUS  
DEFINITION  
AL546878 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CS0D1026YK10 5-PRIME, mRNA sequence.  
VERSION  
AL546878  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE  
1 (bases 1 to 951)  
AUTHORS  
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
TITLE  
Full-length cDNA libraries and normalization  
JOURNAL  
Unpublished (2001)  
COMMENT  
On Feb 15, 2001 this sequence version replaced gi:11268711.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr; Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
10246.f  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?e=CS0D1026BF05QPlc=10246.f.  
Location/Qualifiers  
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/organism="Homo sapiens"  
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/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES  
Source  
Location/Qualifiers  
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/note="1st strand cDNA was primed with a NotI-oligo(dT)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 95.8%; Score 887.4; DB 1; Length 951;  
Best Local Similarity 99.0%; Pred. No. 6e-209;  
Matches 912; Conservative 2; Mismatches 3; Indels 4; Gaps 2;  
QY 4 GCCCATTTCTGTTTACGACGATCGCCAAAGATCATGAATTCGCGAGTGCACACCGCCA 63

Db 32 GCCATTCTGTTTCAAGCCAGTCCGCAAGAAATCATGAAATCCGCACTGGCAGACACCGCA 91  
Qy 64 CCGCCCGCCCGCCCGCCAGCTGCGCTGAAGCGCGCAAGCAGGAGCGGTGGCGCG 123  
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Qy 181 GGGCGCGCGCTGCGCTGCTGAGCAGCAGCAGAGTAAACGTGCTGCTCTACGACATGA 240  
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Qy 421 GCAACCTTCAAGCGCGAGATCAGCGCCCTGAAGCGCGAGCGAGCGTCTCTCGCGAGC 480  
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Qy 481 ATCGCATCTGTGTGCTGAGCGGCTCCCGAGGAGCGCGGAGACCCGAGCATCCAGG 540  
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Db 812 TCACGTTTGCTGCTCTCAGATTTTCTGAGAAAATGCTTTGATTGATATTAATGAT 871  
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Db 931 AATAATTAGATGTGAAAAA 951

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CR600217 939 bp mRNA linear HTC 21-JUL-2004  
LOCUS full-length cDNA clone CS0CAP005Y04 of Thymus of Homo sapiens  
DEFINITION  
(human)  
ACCESSION CR600217  
VERSION CR600217.1 GI:50481024  
KEYWORDS HTC; cNSLT\_cDNA.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 939)  
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished  
REMARK Contact: Peng Liang Email: fliang@life.techn.com URL:  
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
Paradise Avenue  
2 (bases 1 to 939)  
REFERENCE Genoscope.  
AUTHORS Direct Submission  
TITLE Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
COMMENT - Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and BclI sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
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source location/Qualifiers  
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/organism="Homo sapiens"  
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Qy 361 ACTCGGAATCCGAAAGTTGGGACCCCGCGCGCGCGAGGCGTGGCGGCTCCGCTCA 420  
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Qy 421 GCAACCTTCAAGCGCGAGATCAGCGCCCTGAAGCGCGAGCGAGCGTCTCTCGCGAGC 480  
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Qy 541 GGGCAAGAGGAATTAAGTGTCTGTGTGTCTCTCCCGCAAGCGCGCTCGCGAGTGAAGG 600





[illegible]

FEATURES	source
<p><b>AUTHORS</b> NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a></p> <p><b>TITLE</b> National Institutes of Health, Mammalian Gene Collection (MGC)</p> <p><b>JOURNAL</b> Unpublished (1999)</p> <p><b>COMMENT</b> Contact: Robert Straubeberg, Ph.D. Email: cga@rs-remail.nih.gov Tissue Procurement: Invitrogen cDNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLAM12723 row: h column: 12 High quality sequence stop: 705. Location/Qualifiers 1. 1059</p>	<p>/organism="Homo sapiens" /db_type="taxon:9606" /db_xref="taxon:9606" /clone="IMAGE:5728187" /tissue_type="hippocampus" /lab_host="DH10B" /clone_1ib="NIH MGC 124" /note="Organ: brain; Vector: pCMV-Sport6; Site_1: EcorV (destroyed); Site_2: NotI; RNA source male hippocampus, age 27. Library is oligo-dT primed and directionally cloned (EcorV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 0.9-4 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 012."</p>





ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1081)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [gsr@bbs-rcmail.nih.gov](mailto:gsr@bbs-rcmail.nih.gov)  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
<http://image.llnl.gov>  
 Plate: LLM12773 row: 1 column: 18  
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 source anonymous pool of spleen and pancreas from 28 yo  
 male. Library is oligo-dT primed and directionally cloned  
 (EcoRV site is destroyed upon cloning). Average insert  
 size 1.5 kb, insert size range 1-2.5 kb. Library is  
 normalized and enriched for full-length clones and was  
 constructed by C. Gruber (Invitrogen). Research Genetics  
 tracking code 025. Note: this is a NIH-MGC Library."  
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 Query Match 88.6%; Score 820.2; DB 4; Length 1081;  
 Best Local Similarity 95.7%; Pred. No. 2,8e-192;  
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 QY 14 TTTCAGCCAGTGCAGAGATCATGAAAGTCCAGTGGACACCGCCGCGCCG 73  
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 DEFINITION clone CSOD1072Y105 3-PRIME, mRNA sequence.  
 ACCESSION AL576138  
 VERSION AL576138.3 GI:46249018  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 934)  
 L1, W.B., Gruber, C., Jessee, J., and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 COMMENT On Feb 16, 2001 this sequence version replaced gi:31314429.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: [regif@genoscope.cns.fr](mailto:regif@genoscope.cns.fr), Web: [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 10246.f  
 For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?b=CSOD1072AB03NP1&c=10246.f>.  
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ORIGIN sites of the PCWVSPORT 6 vector. Library was normalized."

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Query Match      88.0%; Score 814.8; DB 1; Length 934;
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QY 124 AGGTGTGCGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 180
DB AGGTGTGCGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 707
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QY 301 GCAAGGTGAGATTTCTCCAGCAGCTGATCATCATCATCAGGAGC-CTTCAGTTGAGCTG 359
DB GCAAGGTGAGATTTCTCCAGCAGCTGATCATCATCATCAGTGTGAGTGTGAGCTG 527
QY 360 AACTGGGATCCGAGATTTGGGAGCCCCCGGGGGCGGAGGGCTGCGGCTCGGCTG 419
DB TACTGGGATCCGAGATTTGGGAGCCCCCGGGGGCGGAGGGCTGCGGCTCGGCTG 467
QY 420 AGCACCTTCAACGCGGAGATTCAGCGCGCTGAGCGCGGCGGCGGAGCTTCTCTGCGAGC 479
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QY 720 AGGGGGTGGGATTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 779
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VERSION        CA777979.1 GI:26015854
KEYWORDS
SOURCE
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               Homo sapiens (human)
REFERENCE
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
               1 (bases 1 to 839)
               Lemisha, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
               Hillier, L., Marra, M., Page, D., Wyllie, T., Martin, J., Bilsztain, A.,
               Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J.,
               Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarelis, R.,
               Williams, T., Jackson, Y., and Bowers, Y.
               Endocrine Pancreas Consortium
               Unpublished (2000)
               Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
               Endocrine Pancreas Consortium
               Harvard University, Howard Hughes Medical Institute
               Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
               MA 02138
               Tel: 617-495-1812
               Fax: 617-495-8557
               Email: dmelton@biohp.harvard.edu
               Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
               Washington University Genome Sequencing Center for information on
               obtaining a clone please contact: Dr. Hiroshi Inoue
               (hinoue@im.wustl.edu)
               Seq primer: -40UP from Gibco
               High quality sequence stop: 447.
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   Size-selected on agarose gel. Average insert size ~1kb. 5'
   XhoI site was destroyed after directional cloning.
   Amplified once. Contact information: Hiroshi Inoue, MD,
   Metabolism Div. (Alan Permut Lab), Washington University
   School of Medicine, Box 8127, 660 South Euclid Ave., St.
   Louis, MO 63110, E-mail: hinoue@ingate.wustl.edu, Tel:
   314-362-1916, Fax: 314-747-2692."
ORIGIN
Query Match      87.8%; Score 813.4; DB 6; Length 839;
Best Local Similarity 98.9%; Pred. No. 1.3e-190;
Matches 830; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

QY 84 TCGCGCTGAAGAGCGCGGCAAGACAGCGAGCGGTGCGGCGGAGTGTGCTGTCTGTCT 143
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QY 839 TCGCGCTGAAGAGCGCGGCAAGACAGCGAGCGGTGCGGCGGAGTGTGCTGTCTGTCT 780
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QY 144 GAGCAGACGCGGCGCATTCGCGCGT---CGGGGCGCGCGGGCGCGGCGGCTGCGCGCGT 200
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Qy	441	AGCGCCCTGAGCGCGGAGCGGACATGCTTCTCTGGAGACGATTCGATTTTGTGCTGTA	500
Db	479	AGCGCCCTGAGCGCGGAGCGGACATGCTTCTCTGGAGACGATTCGATTTTGTGCTGTA	420
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LOCUS	AL553031	961 bp	mRNA linear EST 30-MAR-2004
DEFINITION	AL553031 Homo sapiens PLACENTA CON 25-NORMALIZED Homo sapiens cDNA		
ACCESSION	AL553031		
VERSION	AL553031.3	GI:45857801	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 961)		
JOURNAL	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.		
COMMENT	Full-length cDNA libraries and normalization		
	Unpublished (2001)		
	On Feb 15, 2001 this sequence version replaced gi:31274845.		

For more information about this cluster, see <http://www.genoscope.cns.fr/cdna?c=CS0DI072AE03QP1&c=10246.f.>

FEATURES	Location/Qualifiers
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/clone="CSOD1072Y105"
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/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Quarry Match      87.8%; Score 813.2; DB 1; Length 961;
Best Local Similarity 95.7%; Pred. No. 1,5e-190;
Matches 880; Conservative 10; Mismatches 19; Indels 11; Gaps 5

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Query Match	Similarity	97.8%;	Score 813.2;	DB 1;	Length 961;
Best Local	Similarity	95.7%;	Pred. No. 1,5e-190;		
Matches	880;	Conservative	10;	Mismatches	19;
				Indels	11;
				Gaps	5
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QY	64	CCGCCGCCCGGGGGCCCCCAGCTGCGGCTGAAGAGCCGGCAAGACAGCCGTTGGCGGCG	123		
Db	110	CCGCCGCCCGGGGGCCCCCAGCTGCGGCTGAAGAGCCGGCAAGACAGCCGTTGGCGGCG	169		
QY	124	AGGTGATGCGGTCTGTCTGAGCAGACGAGCCATCTCGGCGCTG---CCGGGGCGCCG	180		
Db	170	AGGTGATGCGGTCTGTCTGAGCAGACGAGCCATCTCGGCGCTG---CCGGGGCGCCG	229		
QY	181	GAGCGCGCGCTGCTGCTGCTGAGCAGACAGCAGTAAAGTGTGCTTACGACATGA	240		
Db	230	GAGCGCGCGCTGCTGCTGCTGAGCAGACAGCAGTAAAGTGTGCTTACGACATGA	289		
QY	241	ACGGCTGTACTCACGCTTCAAGAGCTGTGTGCCACCTTGCCCAAGACCGCAAGGTGA	300		
Db	290	ACGGCTGTACTCACGCTTCAAGAGCTGTGTGCCACCTTGCCCAAGACCGCAAGGTGA	349		
QY	301	GCAAGGTGAAGATTCCTCCAGACGTCATCGACTATACAGGGACCTTCAGTTGAGACTGA	360		
Db	350	GCAAGGTGAAGATTCCTCCAGACGTCATCGACTATACAGGGACCTTCAGTTGAGACTGA	409		
QY	361	ACTCGGAATCCGAAGTTGGGAGACCCCGGGGGCCGAGGGCTGCGGATCCGGGCTCCGCTCA	420		
Db	410	ACTCGGAATCCGAAGTTGGGAGACCCCGGGGGCCGAGGGCTGCGGATCCGGGCTCCGCTCA	469		
QY	421	GCACCTTCAAGCGGAGATCAGCGCTCTGAGCGGCCGAGCGGCATAGCTTCTCTGGGAGC	480		
Db	470	GCACCTTCAAGCGGAGATCAGCGCTCTGAGCGGCCGAGCGGCATAGCTTCTCTGGGAGC	529		
QY	481	ATCGCATTTGTGTGCGGAAGCGGCTCCCGCAGGAGCCGGGGAGACCCCAAGCATTCAGG	540		
Db	530	ATCGCATTTGTGTGCGGAAGCGGCTCCCGCAGGAGCCGGGGAGACCCCAAGCATTCAGG	589		
QY	541	GGGCAAGAGGAATTACGTGCTCTGTGGGTTCTCCCCAAAGCGCCTCGCCGATCTTGAGGG	600		
Db	590	GGGCAAGAGGAATTACGTGCTCTGTGGGTTCTCCCCAAAGCGCCTCGCCGATCTTGAGGG	649		
QY	601	AGAACAGAACCGAATCGGCGGCCACTGCGCCCTTAACTGCACTCAGCTGGGGCTGAGCTT	660		
Db	650	AGAACAGAACCGAATCGGCGGCCACTGCGCCCTTAACTGCACTCAGCTGGGGCTGAGCTT	709		
QY	661	GAGGACATCGGAGAGAGAGGGCGCTCTCTGCAACCTTACTATACACCAAGACTTGA	720		
Db	710	GAGGACATCGGAGAGAGAGGGCGCTCTCTGCAACCTTACTATACACCAAGACTTGA	769		
QY	721	GGGGGTGGGATTCACACTGCTGTGTTCTATTATTTTGAAGAAGCAGACATTTTAAAAATGG	780		
Db	770	GGGGGTGGGATTCACACTGCTGTGTTCTATTATTTTGAAGAAGCAGACATTTTAAAAATGG	828		
QY	781	TCACGTTTGGTCTTCAGATTTTCGAGAGAAATGCTTTGTATTGTATATTAACAATGAT	840		
Db	829	TCACGTTTGGTCTTCAGATTTTCGAGAGAAATGCTTTGTATTGTATATTAACAATGAT	887		
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Db 942 AATAWTTADRTGCGKAAAA 961

Search completed: December 18, 2004, 20:21:47  
Job time : 3377.83 secs

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REFERENCE  
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 982)

TITLE NEUROBLASTOMA-ASSOCIATED REGULATOR GENE  
 JOURNAL Patent: WO 9313205-A 1 08-JUL-1993;  
 FEATURES location/Qualifiers  
 source 1. .982

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1. .123
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ORIGIN 971. . 976
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Db	40	GATCCTGCACACAGGAACTTCAAGCACTCACTCTTTGATTTCTTTCTCTTTGGG	99		
QY	344	GCACCTCTGAGTCACTATCCCCAGCATGAAGGCGCTTGAGCCCGGTCGCGCTTACAG	403		
Db	100	GCACCTCTGAGTCACTATCCCCAGCATGAAGGCGCTTGAGCCCGGTCGCGCTTACAG	159		
QY	404	GCGGTGTGTGCTGCTGCGGAACGAGTGTGCGCATTCGCCCGGGGCGGAGGAAGGCCG	463		
Db	160	GCGGTGTGTGCTGCTGCGGAACGAGTGTGCGCATTCGCCCGGGGCGGAGGAAGGCCG	219		
QY	464	GCACTGAGAGAGCCGCTGAGCTTGTGTGACGACATGAACCACTGTACTTCCGCGTGGG	523		
Db	220	GCAGCTGAGAGCCGCTGAGCTTGTGTGACGACATGAACCACTGTACTTCCGCGTGGG	279		
QY	524	GAACCTGATACCCGAGTCCCGAGAGGCACTAGCTTAAACGAGTGAATCTTACAGCG	583		
Db	280	GAACCTGATACCCGAGTCCCGAGAGGCACTAGCTTAAACGAGTGAATCTTACAGCG	339		
QY	584	GTCACTGACTCAATCTTGACCTGAGGTAATCTTGCGCCAGGCGACGCCCTGAGACCCCT	643		
Db	340	GTCACTGACTCAATCTTGACCTGAGGTAATCTTGCGCCAGGCGACGCCCTGAGACCCCT	399		
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QY	704	GACAAAGAGAGCTTTTGTGCACTGACTGCGCCGTGTCTTGACAACCTCCAGAACGAGGTGC	763		
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QY	824	TGGGCCCCAACTTGTGCGCTTGCCCACTTGACTTACAAATCCCTTCTGTGAGACTAAAC	883		
Db	580	TGGGCCCCCACTTGTGCGCTTGCCCACTTGACTTACAAATCCCTTCTGTGAGACTAAAC	639		

QY	884	TGGTGCTCAGAGACCGAAGGACTGTGTAACCTGTGACCTGGAAGAGCCAGAGCTTACCTCTGGC	943
Dp	640	TGTGTCTCAGAGACCGAAGAGACTGTTAACCTGTGTGACCTGGAAGAGCCAGAGCTTACCTCTGGC	699
QY	944	CACCAAGTGGGCGACGTCAACCTGTGCTCCACCCACCACCCCAAGTGTGAAGTCTTTTCAG	1000
Dp	700	CACCAAGTGGGCGACGTCAACCTGTGCTCCACCCCA - CCCCAGTGTCAAGTCTTTTCAG	758
QY	1004	AGCGTGAAGGTGTGGAAGAGAGTGCTGTCTCCAAACTATGACCAAGCGCGCGCAGAGCT	1063
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Dp	819	GGCTCTCTGCTCTCCTTGAGAAAGGTTCTGTGTGCTGCTGATTTTATGTAACCTATATATAG	878
QY	1123	GTATATAGGTTTGTGACCTTTTTCACAGGAAGGTGACTTCTGTAAACAATCGCATGTAT	1182
Dp	879	GTATATAGGTTTGTGACCTTTTTCAC - GGAAGGTGACTTCTGTAAACAATCGCATGTAT	937
QY	1183	ATTAACCTTTTATATAAGTT 1203	
Dp	938	ATTAACCTTTTATATAAGTT 958	

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	RESULT 4
159693	Sequence 1 from patent US 565418.	159693	159693.1	GI:2478325	159693
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					DNA
					linear
					PAT 07-OCT-1997

SOURCE	Unknown.
ORGANISM	Unknown.
DISTRIBUTION	Unclassified.

REFERENCE	1 (bases 1 to 982)
AUTHORS	Billmeier, W. and Weith, A.
TITLE	Neuroblastoma-associated regulator gene
JOURNAL	Patent: US 5651188-A 1 05-AUG-1997,
FEATURES	Location/Qualifiers
source	1. 982

**ORIGIN**

Query Match	71.2%	Score 856.2	DB 6	Length 982
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				Indels 3
				Gaps 3
QY	284	GAGCGTCGCGCGTGTGACAGTCACTGTAAGCGGACCTTTTGGTTTCTTTCTTTGGG	343	
Db	40	GATCTCGACACACGGGAACTCACAGACCTCACTTCTTTGGTTTCTTTCTTTGGG	99	
QY	344	GCACTCTTGAATCACTCCCGAGCATGAAGCGCTGAGCCGGTGGCGGCTGTACAG	403	
Db	100	GCACCTTGAATCACTCCCGAGCATGAAGCGCTGAGCCGGTGGCGGCTGTACAG	159	
QY	404	GGGGTGTGCTGCTGTGCGAAACGACGTCTTGGCATGCCCGGCGCGAGGAAAGGCCG	463	
Db	160	GGGGTGTGCTGCTGTGCGAACGACGTCTTGGCATGCCCGGCGCGAGGAAAGGCCG	219	
QY	464	GCAGCTGAGGAGCGGCTGAGCTTGTGCGAACGACATGAACAATTGTACTCCCGCTGGG	523	
Db	220	GCAGCTGAGGAGCGGCTGAGCTTGTGCGAACGACATGAACAATTGTACTCCCGCTGGG	279	
QY	524	GAACTGTGTAACCGGAGTCCCGAGAGGCACTCAAGCTTACGAGGTGAATCTCAAGGC	583	
Db	280	GAACTGTGTAACCGGAGTCCCGAGAGGCACTCAAGCTTACGAGGTGAATCTCAAGGC	339	
QY	584	GTCAATCGAATCAATTCTTCGACTTGCAGGTATGTCCTGGCCGAGCAGCCCTGACCCCT	643	
Db	340	GTCAATCGAATCAATTCTTCGACTTGCAGGTATGTCCTGGCCGAGCAGCCCTGACCCCT	399	



QY 644 GATGGCCCCCAGCTTCCCATCCAGACAGCGAGCTCGCTCGGAACTTGTCTCCAC 703  
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QY 704 GACAAAGAGAGCTTTTGGCACTGACTCGGCGGTCTGACACCTTCAGAACGAGGTGC 763  
DB 460 GACAAAGAGAGCTTTTGGCACTGACTCGGCGGTCTGACACCTTCAGAACGAGGTGC 519  
QY 764 TGGCGCCGCTTCTGCTTGGGACCCCGGAACTCTCTCGGAAAGCCGAGCGGGA 823  
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QY 884 TGGTCTCAGAGCGAG 943  
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DB 879 GATATAGAGTTTGTATCTTTTACAGGAAAGTGTCTGTATCAATGCGATAT 937  
QY 1183 ATTAACTTTTATTAAGTT 1203  
DB 938 ATTAACTTTTATTAAGTT 958

RESULT 5  
172140 982 bp DNA linear PAT 03-APR-1998  
DEFINITION Sequence 1 from patent US 5683878.  
ACCESSION 172140  
VERSION 172140.1 GI:3008279  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 982)  
AUTHORS Ellmeier,W. and Weith,A.  
TITLE Neuroblastoma-associated regulator gene  
JOURNAL Patent: US 5683878-A 1 04-NOV-1997;  
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QY 284 GAGCGTGGCGGCTTGACAGTGTACAGGAGCTTCTTTGTTTCTTTCTTTGGG 343  
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QY 344 GACCTCTGAGACTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 403  
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DB 580 TGGGCCCCCACTTCGCTCGCCCACTTGAATTCCTTCCTGAGACCTAAACC 639  
QY 884 TGGTCTCAGAGCGAG 943  
DB 640 TGGTCTCAGAGCGAG 699  
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DB 700 CACCAAGCTGGGAG 758  
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DB 879 GATATAGAGTTTGTATCTTTTACAGGAAAGTGTCTGTATCAATGCGATAT 937  
QY 1183 ATTAACTTTTATTAAGTT 1203  
DB 938 ATTAACTTTTATTAAGTT 958

RESULT 6  
AX663639 982 bp DNA linear PAT 22-MAR-2003  
LOCUS AX663639  
DEFINITION Sequence 14 from Patent WO02097127.  
ACCESSION AX663639  
VERSION AX663639.1 GI:29163847  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
REFERENCE 1  
AUTHORS Oellers,N., Gehrmann,M., Kalibbie,H., Hall,R., Schulze,T. and Kroegel,C.  
TITLE Genes and proteins for prevention, prediction, diagnosis, prognosis and treatment of chronic lung disease

JOURNAL Patent: WO 02097127-A 14 05-DEC-2002;  
Bayer Aktiengesellschaft (DE)  
FEATURES Location/Qualifiers  
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Query Match 71.2%; Score 856.2; DB 6; Length 982;  
Best Local Similarity 97.7%; Pred. No. 1.7e-188;  
Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

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Qy 404 GCGGTGTCTGCTGTGTGGAAGCAAGTCTGAGCCATGCGCCCGGGCGGAGAGAGCGCG 463  
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Qy 464 GCGGTGTGAGAGCGCGCTGAGCTTGTGAGAGATGAGATGAGCACTGCTACTCCGCGCTGCGG 523  
Db 220 GCGGTGTGAGAGCGCGCTGAGCTTGTGAGAGATGAGATGAGCACTGCTACTCCGCGCTGCGG 279  
Qy 524 GAACTGTGATCCCGAGTCCCGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAG 583  
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Db 400 GATGCGCCCACTTCTGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAG 459  
Qy 704 GACAAAGAGAGCTTTTGGCTGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 763  
Db 460 GACAAAGAGAGCTTTTGGCTGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 519  
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Db 938 ATTAACCTTTTATTAAGTT 958

RESULT 7  
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DEFINITION H.sapiens heir-1 mRNA for helix-loop-helix protein.  
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VERSION X66924.1 GI:395337  
KEYWORDS helix-loop-helix protein.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 982)  
Elmeier, W., Aguzzi, A., Kleiner, E., Kurzbauner, R. and Weith, A.  
Mutually exclusive expression of a helix-loop-helix gene and N-myc  
in human neuroblastomas and in normal development  
EMBO J. 11 (7), 2563-2571 (1992)  
JOURNAL 92331608  
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PUBMED  
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ORIGIN  
Query Match 71.2%; Score 856.2; DB 9; Length 982;  
Best Local Similarity 97.7%; Pred. No. 1.7e-188;  
Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

Qy 284 GAGCGTGGCGCGCTGGAGGTCAGTCACTGAGCGGAGCTTTTGGTTTCTTCTTTGGG 343  
Db 40 GATCTGACACACGGGAACCTCAGACACCTCACTTTTGGTTTCTTCTTTGGG 99  
Qy 344 GCACCTTGAGATCACTCCCGAGATGAAGCGCTGAGCGCGCTGCTACGAG 403  
Db 100 GCACCTTGAGATCACTCCCGAGATGAAGCGCTGAGCGCGCTGCTACGAG 159  
Qy 404 GCGGTGTCTGCTGTGTGGAAGCAAGTCTGAGCCATGCGCCCGGGCGGAGAGAGCGCG 463  
Db 160 GCGGTGTCTGCTGTGTGGAAGCAAGTCTGAGCCATGCGCCCGGGCGGAGAGAGAGCGCG 219  
Qy 464 GCGGTGTGAGAGCGCGCTGAGCTTGTGAGAGATGAGATGAGATGAGATGAGATGAGATGAGAG 523  
Db 220 GCGGTGTGAGAGCGCGCTGAGCTTGTGAGAGATGAGATGAGATGAGATGAGATGAGATGAGAG 279  
Qy 524 GAACTGTGATCCCGAGTCCCGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 583  
Db 280 GAACTGTGATCCCGAGTCCCGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 339  
Qy 584 GTGATGAGATCACTTCTGAGCTGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 643  
Db 340 GTGATGAGATCACTTCTGAGCTGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 399  
Qy 644 GATGCGCCCACTTCTGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAG 703

Db 400 GATGGCCCCACCTTCCATCCAGACAGCGAGCTGGCTCCGGAACTTGTATCTTCCAAAC 459  
Qy 704 GACAAAAGAGCTTTTGGCCACTGACTCGCGCCGTGCTCTGACACCTCCAGAACGCAAGTGC 763  
Db 460 GACAAAAGAGCTTTTGGCCACTGACTCGCGCCGTGCTCTGACACCTCCAGAACGCAAGTGC 519  
Qy 764 TGGCGCCGCTTGTGCTGGGACCCCGGGAACTCTCCGCGCGAAGCCGGAGCGGAGGGA 823  
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Qy 824 TGGCGCCCACTTCGCGCCCTGCCCACTTGACTTCACCAATCCCTTCTGAGACTAAAC 883  
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Qy 884 TGGCTCTCAGAGCGAAGACTGTGAATCTTGACCTGGAAGCCAGACTAGCTCTGCG 943  
Db 640 TGGCTCTCAGAGCGAAGACTGTGAATCTTGACCTGGAAGCCAGACTAGCTCTGCG 699  
Qy 944 CACCGAGTGGGGAGAGTCACTGCTGCCCAACCCCACTTCTAAGTCTTTTCA 1003  
Db 700 CACCGAGTGGGGAGAGTCACTGCTGCCCAACCCCACTTCTAAGTCTTTTCA 758  
Qy 1004 AGCGTGAAGTGTGGAAGAGTGTGCTCTCCAACTATGCGCAAGCGCGGAGAGCT 1063  
Db 759 AGCGTGAAGTGTGGAAGAGTGTGCTCTCCAACTATGCGCAAGCGCGGAGAGCT 818  
Qy 1064 GGTCTTGTGCTCTCTTGAGAAAGTTCGTGCGCTGATTTATGAATCTATATAG- 1122  
Db 819 GGTCTTGTGCTCTCTTGAGAAAGTTCGTGCGCTGATTTATGAATCTATATAG 878  
Qy 1123 GATATAGTTTTGTACCTTTTTCAGGGAAGTGTCTGTGAACAATGCGATGAT 1182  
Db 879 GATATAGTTTTGTACCTTTTTCAG- GGAAGTGTACTTGTGAACAATGCGATGAT 937  
Qy 1183 ATTAACTTTTATATAAGTT 1203  
Db 938 ATTAACTTTTATATAAGTT 958

RESULT 8  
BV178372/c 957 bp DNA linear STS 10-JUN-2004  
LOCUS BVL178372 Human DNA (Sequenom) Homo sapiens STS genomic, sequence  
DEFINITION tagged site.  
ACCESSION BVL178372  
VERSION BVL178372.1 GI:48014698  
KEYWORDS STS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 957)  
AUTHORS Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,  
Cantor,C.R. and Braun,A.  
TITLE Large-scale validation of Single Nucleotide Polymorphisms in Gene  
Regions  
JOURNAL Genome Res. (2004) In press  
COMMENT Contact: Andreas Braun  
Pharmaceuticals division  
Sequenom, Inc.  
3595 John Hopkins Court, San Diego, CA 92121, USA  
Tel: 18582029018  
Fax: 18582029020  
Email: abraun@sequenom.com  
Primer A: No primer sequence submitted  
Primer B: No primer sequence submitted  
STS size: 957.

FEATURES  
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Location/Qualifiers  
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Query Match 71.0%; Score 854; DB 11; Length 957;  
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Matches 890; Conservative 1; Mismatches 10; Indels 3; Gaps 3;

Qy 302 GGTCACTGTAC- GACTCTTTTGGTTTCTTTCTTTGGGCACTCTGACTACT 360  
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Qy 361 CCCGAGATGAAGGGCTGAGACCCCGGTGCGGCTGCTACAGAGGGGTGTGCTGTC 420  
Db 889 CCCGAGATGAAGGGCTGAGACCCCGGTGCGGCTGCTACAGAGGGGTGTGCTGTC 830  
Qy 421 GGAAAGCACTGTGCGCATGCGCCGGGGCGAGAGGAGGCGGAGCTGAGAGCCGCT 480  
Db 829 GGAAAGCAAGTGTGCGCATGCGCCGGGGCGAGAGGAGGCGGAGCTGAGAGCCGCT 770  
Qy 481 GAGCTTGTGAGCGACATGAACCACTGTACTCCGCTGCGGGAATGTAACCGGAGT 540  
Db 769 GAGCTTGTGAGCGACATGAACCACTGTACTCCGCTGCG- GGAATGTATCCGGAAT 711  
Qy 541 CCCGAGAGCACTAGCTTGAAGCAAGTGTGAATCTTAAGAGGCTCATGACTACTTCT 600  
Db 710 CCCGAGAGCACTAGCTTGAAGCAAGTGTGAATCTTAAGAGGCTCATGACTACTTCT 651  
Qy 601 CGACTGTGAGGATGCTGTGCGGAGCGAGCCCGCTGAGCCCTGATGGCCCCCACTTCC 660  
Db 650 CGACTGTGAGGATGCTGTGCGGAGCGAGCCCGCTGAGCCCTGATGGCCCCCACTTCC 591  
Qy 661 CATCCAGACAGCCGAGCTGCTCGGAACTTGTCACTCCACGACAAAGAGAGCTTTTG 720  
Db 590 CATCCAGACAGCCGAGCTGCTCGGAACTTGTCACTCCACGACAAAGAGAGCTTTTG 531  
Qy 721 CCACTGACTCGGCGGTGCTGACCACTTCAGAAAGCAAGTGTGCGCCGCTTGTGCT 780  
Db 530 CCACTGACTCGGCGGTGCTGACCACTTCAGAAAGCAAGTGTGCGCCGCTTGTGCT 471  
Qy 781 GGGACCCCGGGAACTCTCTGCGGGAAGCGGAGCGGAGGAGTGGGCCCAACTTGGCC 840  
Db 470 GGGACCCCGGGAACTCTCTGCGGGAAGCGGAGCGGAGGAGTGGGCCCAACTTGGCC 411  
Qy 841 CTGCCCACTTGAATTCACCAATCCCTTCTGAGACTAAACTGTGTCTCAGAGCGAA 900  
Db 410 CTGCCCACTTGAATTCACCAATCCCTTCTGAGACTAAACTGTGTCTCAGAGCGAA 351  
Qy 901 GAGCTGTGAATCTTGAGCTTGAAGAGCGAGCTAGCTGTGCGCACAGTGGGAGAGT 960  
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Qy 961 CACCTGTGCCACCCCAACCCCAAGTCTTAAGCTTTTTCAGAGCGTGGAGGTGGA 1020  
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Qy 1021 GAGGTGCTGTCTTCCAACTATGCGCAAGGCGCGGAGAGTGTCTTGTGCTCTT 1080  
Db 230 GAGGTGCTGTCTTCCAACTATGCGCAAGGCGCGGAGAGTGTCTTGTGCTCTT 171  
Qy 1081 GAGAAAGTGTCTGTGCGCTGATTTATGAATCTATATAG- GATATAGTTTTGTAC 1139  
Db 170 GAGAAAGTGTCTGTGCGCTGATTTATGAATCTATATAGAGTATATAGTTTTGTAC 111  
Qy 1140 CTTTATTACAGGAAAGTGTCTGTGAACAATGCGATGTATATAACTTTTATAA 1199  
Db 110 CTTTATTACAGGAAAGTGTCTGTGAACAATGCGATGTATATAACTTTTATAA 51  
Qy 1200 AGTT 1203  
Db 50 AGTT 47



TITLE Genes involved in osteogenesis, and methods of use  
JOURNAL Patent: WO 02081745-A 136 17-OCT-2002;  
Aventis Pharma S.A. (FR)

FEATURES  
source  
Location/Qualifiers  
1. 2481  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
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ORIGIN

Query Match 55.2%; Score 663.8; DB 6; Length 2481;  
Best Local Similarity 99.7%; Pred. No. 1.1e-143;  
Matches 665; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCTGGGGGTGCTGCCAGAGAAAGCAATTCTGGAAGTTAATGGTTTGAAGTATTCTT 60  
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QY 61 AAATCCTTGCTGGCGAGAGAGCGCGCTCTCCCGGTATCCAGCGCTTCTCATTTCTTGA 120  
DB 432 AAATCCTTGCTGGCGAGAGAGCGCGCTCTCCCGGTATCCAGCGCTTCTCATTTCTTGA 491  
QY 121 ATCCCGCGGTCCCGCGGTCTTCCGCGCTCAGACCAAGCCGAGAGAGCTGTTTGCATTTTAA 180  
DB 492 ATCCCGCGGTCCCGCGGTCTTCCGCGCTCAGACCAAGCCGAGAGAGCTGTTTGCATTTTAA 551  
QY 181 GCGGCGTGTGAACGCCAGAGCGCGCGCGGCGGCGGCGAGGCGGCGCATTTTGAATATA 240  
DB 552 GCGGCGTGTGAACGCCAGAGCGCGCGCGGCGGCGGCGAGGCGGCGCATTTTGAATATA 611  
QY 241 GAGGGGTGCTTCCAGGCGAGGCTTATAGTACACGCGCGGCGAGCGGCGGCGGTTGC 300  
DB 612 GAGGGGTGCTTCCAGGCGAGGCTTATAGTACACGCGCGGCGAGCGGCGGCGGTTGC 671  
QY 301 AGGTCACTGTAGCGGACCTTTTGGTTTCTTTTCTTTTGGGAGCACTCTGAGTCACT 360  
DB 672 AGGTCACTGTAGCGGACCTTTTGGTTTCTTTTCTTTTGGGAGCACTCTGAGTCACT 731  
QY 361 CCCGACATGAAGCGCTGAGCGCGGTGCGCGCTGCTACGAGCGGCTGTGCTGCTGTC 420  
DB 722 CCCGACATGAAGCGCTGAGCGCGGTGCGCGCTGCTACGAGCGGCTGTGCTGCTGTC 791  
QY 421 GGAAGCGAGTCTGGCGCATATGCGCGGCGCGAGAGAGGCGCGGAGCTGAGAGAGCGCT 480  
DB 792 GGAAGCGAGTCTGGCGCATATGCGCGGCGCGAGAGAGGCGCGGAGCTGAGAGAGCGCT 851  
QY 481 GAGCTTGTGAGAGCATGAACAACACTGTAATCCGCGCTGCGGAGAACTGGTACCGGAGT 540  
DB 852 GAGCTTGTGAGAGCATGAACAACACTGTAATCCGCGCTGCGGAGAACTGGTACCGGAGT 911  
QY 541 CCCGAGAGGCACTCAGCTTATGCGAGGTGAGAAATCTTACAGCGCGTCTATGACTACATTCT 600  
DB 912 CCCGAGAGGCACTCAGCTTATGCGAGGTGAGAAATCTTACAGCGCGTCTATGACTACATTCT 971  
QY 601 CGAAGCTGAGAGTATGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660  
DB 972 CGAAGCTGAGAGTATGCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1031  
QY 661 CATCCAG 667  
DB 1032 CATCCAG 1038

RESULT 11  
LOCUS HS1D3HLH 2481 bp DNA linear pri 21-APR-1995  
DEFINITION H.sapiens Id3 gene for HLH type transcription factor.  
ACCESSION X73428.1 GI:313212  
VERSION X73428.1  
KEYWORDS early response gene; transcriptional factor.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
1 Deed,R.W., Hirose,T., Mitchell,E.L., Santibanez-Koref,M.F. and Notton,J.D.

TITLE  
JOURNAL Gene 151 (1-2), 309-314 (1994)

MEDLINE  
95129881

PUBMED  
7828896

REFERENCE  
2 (bases 1 to 2481)

AUTHORS  
Deed,R.

TITLE  
JOURNAL Direct Submission  
Submitted (18-JUN-1993) R. Deed, Paterson Institute for Cancer Research, Dept of Gene Regulation, Christie Hospital NHS Trust, Wilmslow Road, Manchester, M20 9BX, UK

FEATURES  
source  
Location/Qualifiers  
1. 2481  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
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/chromosome="1"  
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/tissue\_type="peripheral blood"  
/clone\_id="pcos2emb1"  
/genome="hg17"  
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ORIGIN

Query Match 55.2%; Score 663.8; DB 9; Length 2481;  
Best Local Similarity 99.7%; Pred. No. 1.1e-143;  
Matches 665; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCTGGGGGTGCTGCCAGAGAAAGCAATTCTGGAAGTTAATGGTTTGAAGTATTCTT 60  
DB 372 GATCTGGGGGTGCTGCCAGAGAAAGCAATTCTGGAAGTTAATGGTTTGAAGTATTCTT 431  
QY 61 AAATCCTTGCTGGCGAGAGAGCGCGCTCTCCCGGTATCCAGCGCTTCTCATTTCTTGA 120  
DB 432 AAATCCTTGCTGGCGAGAGAGCGCGCTCTCCCGGTATCCAGCGCTTCTCATTTCTTGA 491



repeat\_region 9606..9819  
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/note="L1MA10 repeat: matches 6249..6322 of consensus"  
repeat\_region 9927..9990  
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repeat\_region 9991..10303  
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repeat\_region 11159..11466  
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repeat\_region 11493..11748  
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repeat\_region 12196..12256  
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repeat\_region 12257..12541  
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repeat\_region 17330..17399  
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repeat\_region 17441..17747  
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repeat\_region 17807..17959  
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repeat\_region 18167..18356  
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repeat\_region 18357..18657  
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repeat\_region 18789..19101  
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Query Match 54.3%; Score 652.8; DB 9; Length 129722;  
Best Local Similarity 99.6%; Pred. No. 5e-141;  
Matches 665; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GATCGGGGCTCCCGAGAAAAGCAAAATCTGGAATTAATGTTTGAATGCTT 60  
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QY 61 AAATCTTGCTGGCGAGAGCGCGCTCTCCCGGATACAGCGCTTCCTGATTTGA 120  
DB 109498 AAATCTTGCTGGCGAGAGCGCGCTCTCCCGGATACAGCGCTTCCTGATTTGA 109439

QY 121 ATCCGGGCTCCCGGCTTTGGCGTACAGACCGGAGAGAGCTTGTGCAATTTAA 180  
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QY 241 GAGCGTCTTCCAGGAGGCTCTAATAAGACCGCGCGCGAGCGTGGCGCGTTC 300  
DB 109318 GAGCGTCTTCCAGGAGGCTCTAATAAGACCGCGCGCGAGCGTGGCGCGTTC 109259

QY 301 AGGTCACTGAGC-GGACTTTTGTGTTTCTTTTGGGGACCTTGACTAC 359  
DB 109258 AGGTCACTGAGCGGAACTTTTGTGTTTCTTTTGGGGACCTTGACTAC 109199

QY 360 TCCCGAGATGAAGCGGTGAGCCCGGCGCGCGGTGTAAGAGCGGTGTCGCTGT 419  
DB 109198 TCCCGAGATGAAGCGGTGAGCCCGGCGCGGTGTAAGAGCGGTGTCGCTGT 109139

QY 420 CGAAGCGAGTCTGGCCATCCCGCGGCGCGAGGAGAGCGCGCACTGAGAGCGCG 479  
DB 109138 CGAAGCGAGTCTGGCCATCCCGCGGCGCGAGGAGAGCGCGCACTGAGAGCGCG 109079

QY 480 TGAGCTTCTGAGACGATGAACAACCTGCTACTCCCGCTTGCGGGAATGTAACCGAG 539  
DB 109078 TGAGCTTCTGAGACGATGAACAACCTGCTACTCCCGCTTGCGGGAATGTAACCGAG 109019

QY 540 TCCGAGAGGACCTAGCTTAAGCAAGGTAATCTTAAGAGCGGTATCGACTCATTC 599  
DB 109018 TCCGAGAGGACCTAGCTTAAGCAAGGTAATCTTAAGAGCGGTATCGACTCATTC 108959

QY 600 TCGACCTGAGATGATCTGGCGGAGCGCGCTGAGACCCCTGATGAGCCCACTTC 659  
DB 108958 TCGACCTGAGATGATCTGGCGGAGCGCGCTGAGACCCCTGATGAGCCCACTTC 108899



QY 660 CCATCCAG 667  
 Db 108898 CCATCCAG 108891

RESULT 13  
 MUSH462  
 LOCUS  
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 accession  
 version  
 keywords  
 source  
 organism

MUSH462  
 Mouse helix-loop-helix protein (id related) mRNA, complete cds.  
 M60523.1 GI:193872  
 growth factor-inducible protein; helix-loop-helix protein.  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 Chisley, B.A., Sanders, L.K., Lau, L.F., Copeland, N.G., Jenkins, N.A. and Nathans, D.  
 An id-related helix-loop-helix protein encoded by a growth factor-inducible gene  
 Proc. Natl. Acad. Sci. U.S.A. 88 (5), 1815-1819 (1991)

JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT  
 FEATURES

Original source text: Mouse, cDNA to mRNA.  
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ORIGIN  
 Chromosome 4.

Query Match 38.4%; Score 462; DB 10; Length 969;  
 Best Local Similarity 76.9%; Pred. No. 9,6e-97;  
 Matches 695; Conservative 0; Mismatches 165; Indels 44; Gaps 9;

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 Db 88 TAGGAGCGGTGTGCTGCTGCGAGCGAGTCTGCGCATCGCGCGCGAG 147

QY 458 GGGCGGAGCTGAGGAGCGCGTGAAGTCTGAGCAATGAACCACTGCTACCG 517  
 Db 148 AGCCCGTGAGCGAGGAGCGCTTAGCTCTTGGACCAATGAACCACTGCTACCG 207

QY 518 CTGGCGGAATGTAACCGGAGTCCCGAGGCGCACTGAGTACCGCGTGAATCTTA 577  
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QY 578 CAGGCGCTGATGACTATCTTGAAGTCTGAGTCTGAGCGAGCGCGCTTGA 637  
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QY 638 CCCCCTGATGGCCCGACCTTCCCATGCAACGCGAGTGGCTTCCGGAATCTGTATC 697

Db 328 CCCCCGAGCGTCCCATCTCCCATCCAGACAGTCACTCTCCGGAATCTGTATC 387  
 QY 698 TCACAAGCAAAAGAGCTTTTGGCACTGAGTCCGCGCTGTCTGACACCTCGAAGCG 757  
 Db 388 TCACAAGCAAAAGAGCTTTTGGCACTGAGTCCGCGCTGTCTGACACCTCGAAGCG 445

QY 758 AGTGTCTGCGCGCTTCTGCTGCGAGCGCGGAGTCTGAGTCTGAGTCTGAGTCT 799  
 Db 446 AGTGTCTGCGCGCTTCTGCTGCGAGCGCGGAGTCTGAGTCTGAGTCTGAGTCT 505

QY 800 CTGGCGGAAGCTGAGCGAGGAGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 858  
 Db 506 CAGCGGAGCGCTGAGCGAGGAGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 565

QY 859 CAATTCCTTCTGAGAGCTAAACCTGTCTGAGAGCGAGAGAGAGAGAGAGAGAGAG 918  
 Db 566 CTGAAGCTAAGCTCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAG 625

QY 919 CTGAAGAGCGAGCTGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCT 978  
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QY 979 CCCCCAGTCTTAG--GTCTTTTCAAGCGCTGAGAGTGTGAG-- 1021  
 Db 684 ACTAAGCTTAAAGAGCTGAGTCTTCCGAGAAATGGGAGTGTGAGAGGAGGAGGAG 743

QY 1022 -GAGTGTCTCTCTCCAACTATGCCAGGCGCGAGAGCTGCTCTGCTCTCTCT 1080  
 Db 744 CGAGTGTCT 803

QY 1081 GAGAAAGCTTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1139  
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QY 1140 CTTTCTTACGAGAGAGTGAATCTGTAACAATGAGTATATTAATCTTTATTA 1199  
 Db 863 CTTTCTTACGAGAGAGTGAATCTGTAACAATGAGTATATTAATCTTTATTA 921

QY 1200 AGTT 1203  
 Db 922 AGTT 925

RESULT 14  
 BC064658  
 LOCUS  
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 version  
 keywords  
 source  
 organism

BC064658  
 Rattus norvegicus inhibitor of DNA binding 3, dominant negative helix-loop-helix protein, mRNA (cDNA clone MGC:72531 IMAGE:5623701), complete cds.  
 BC064658  
 BC064658.1 GI:40555866  
 MGC  
 Rattus norvegicus (Norway rat)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 1 (bases 1 to 983)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ushed, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Hale, S., Garcia, A.M., Gay, L.J., Hilyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hilyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,



Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Buterfield, Y.S., Krzywinski, M.I., Skalske, U., Small, D.E., Schermer, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

2 (bases 1 to 983)  
12477932

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Strausberg, R.  
Direct Submission  
Submitted (22-DEC-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapdb-r@mail.nih.gov](mailto:cgapdb-r@mail.nih.gov)  
Tissue Procurement: Dr. Maarten Bosland, NYU  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@nih.gov](mailto:nisc_mgc@nih.gov)  
Akhter, N., Ayala, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Lalic, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stenlidop, S., Thomas, P.J., Touchman, J.W., Tsougenou, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: <http://image.liml.gov>  
Series: IRAX Plate: 137 Row: P Column: 16  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6961073.  
Location/Qualifiers

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ORIGIN  
Query Match 38.3%; Score 460.4; DB 10; Length 983;  
Best Local Similarity 77.5%; Pred. No. 2.3e-96;  
Matches 688; Conservative 0; Mismatches 156; Indels 44; Gaps 9;

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DB 27 CAACCTCCAACTGAAGCGCTGAGCCCGGTGCGGCTGCTACGAGCGGTGCTGCC 86  
QY 417 TGTGGAACGCACTGTGCGCATGCGCGGCGGAGGAGGCGCGGAGCTGAGAGC 476  
DB 87 TGTGGAACGCACTGTGCGCATGCGCGGCGGAGGAGGCGCGGAGCTGAGAGC 146  
QY 477 CGCTAGCTGTGAGCAGACATGAACCACTGTACTCCCGCTGCGGGAACCTGATCCG 536  
DB 147 CGCTAGCTGTGAGCAGACATGAACCACTGTACTCCCGCTGCGGGAACCTGATCCG 206  
QY 537 GAGTCCGAGAGGCACTGAGCTTACGAGTGAATCTTACAGGCGCTGATGACTACA 596  
DB 207 GAGTCCGAGAGGCACTGAGCTTACGAGTGAATCTTACAGGCGCTGATGACTACA 266  
QY 597 TTTCTGACCTGAGGTAAGTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 656  
DB 267 TTTCTGACCTGAGGTAAGTCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 326  
QY 657 TTTCCATCATGACAGAGCGGAGCTGCTCGGGAATCTGTATCTTCAACGACAAAGAGCT 716  
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QY 717 TTTGACATGACTGCGGCGGTGCTGACACCTCCAGAACGACAGTGTGCGCGGCTTCT 776  
DB 387 TTTGACATGACTGCGGCGGTGCTGACACCTCCAGAACGACAGTGTGCGCGGCTTCT 444  
QY 777 GCTTGGAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 825  
DB 445 GCTTGGAGCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 504  
QY 826 GGGCCCAACTTGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTG 883  
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QY 884 TGTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 941  
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DB 625 GTCACGAGCTGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 684  
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DB 685 TTTTTCGAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 744  
QY 1038 AACTATGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1097  
DB 745 CACACTGCGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 804  
QY 1098 CCTGATTTATGAACTGATATATAG-GTATATAGTTTGTACTTTTATTA-GGAG 1155  
DB 805 CCTGATTTATGAACTGATATATAG-GTATATAGTTTGTACTTTTATTA-GGAG 863  
QY 1156 GTGACTTTCTGTAACAATGCGATGTATATTAACCTTTTATTAAGTT 1203  
DB 864 GTGACTTTCTGTAACAATGCGATGTATATTAACCTTTTATTAAGTT 911

RESULT 15  
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LOCUS CFA271644  
DEFINITION Canis familiaris mRNA for ID3 protein (ID3 gene).  
ACCESSION AJ271644  
VERSION AJ271644.1 GI:6782310  
KEYWORDS Id3 gene, Id3 protein.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE  
1

AUTHORS Delau, S., Savonet, V., Behrends, J., Dumont, J. E. and Maenhaut, C.  
 TITLE Study of gene expression in thyrotropin-stimulated thyroid cells by  
 CDNA expression array: ID3 transcription modulating factor as an  
 early response protein and tumor marker in thyroid carcinomas  
 JOURNAL Exp. Cell Res. 279 (1), 62-70 (2002)  
 MEDLINE 22202085  
 PUBMED 12213214  
 REFERENCE 2 (bases 1 to 497)  
 AUTHORS Delau, S.  
 TITLE Direct Submission  
 JOURNAL Submitted (25-JAN-2000) Delau S., Tribin, Institute of  
 Interdisciplinary research, 808 Route de Lemnik, Bruxelles, 1070,  
 BELGIUM

FEATURES  
 source location/Qualifiers

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 ELAPLVISNDKRSFCH"

ORIGIN

Query Match 31.4%; Score 377.2; DB 4; Length 497;  
 Best Local Similarity 89.3%; Pred. No. 5e-77;  
 Matches 418; Conservative 0; Mismatches 48; Indels 2; Gaps 1;

QY 324 TGGTTTCTTCTTCTTGGGCACTCTGACTCTCCAGCATGAAGCGCTGAGCC 383  
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 QY 384 CGGTGGCGGCTGCTAGAGCGGATGTGCTGCTGCGGAGCACTCTGCGCATCGCC 443  
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 QY 444 GGGGCCGAGGAAAGGCGCTGAGAGCGGCTGAGCTTGTGAGCAATGAAC 503  
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 QY 504 ACTGCTACTCCGCGCTGCGGAACTGTATCCCGAGTCCCGAGAGCACTGACTTACC 563  
 Db 212 ACTGCTACTCGGCTTGGGAACTGTATCCCGAGTCCCGAGAGCACTGACTTACC 271  
 QY 564 AGGTGAAATCTTACAGCGCTCATGACTGACTGAGCTGAGGTAAGTCCGAGCG 623  
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 QY 624 AGCGAGCGCGTGAAGCGCTGAGCGCGCTGAGCTTCCATCAAGCAGCGAGCTGCTC 683  
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 Db 392 CGAACTTGTCTCACTCAAGCAAAAGAGCTTGGCACTGAGCTGCGCGGTCTCTGA 449  
 QY 744 CACCTCCAGAGCGAGTGTGCGCGCGCTTGTGCTGAGGACCCCGG 791  
 Db 450 CCGCTCCAGAGCGAGTGTGCGCGCGCTTGTGCTGAGGACCCCGG 497

GenCore version 5.1.6  
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## OM nucleic - nucleic search, using sw model

Run on: December 18, 2004, 13:49:15 ; Search time 660.548 Seconds  
(without alignment)  
9560.323 Million cell updates/sec

Title: US-09-996-529A-5

Perfect score: 1203

Sequence: 1 gatcgggggctcgtccagga.....ttaactttataaagct 1203

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134866 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001s:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1178.4	98.0	1203	6	ABO88115 Human ost
2	1178.4	98.0	1203	10	ADH28990 Human chr
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4	1164.2	96.8	2066	10	ADU56457 Human cdn
5	1162.8	96.7	1300	3	AA121652 Human bre
6	870.2	72.3	3372	8	ACC46300 Human dit
7	856.2	71.2	982	2	AAQ44245 HEIR-1 ge
8	856.2	71.2	982	6	ABO88114 Human ost
9	856.2	71.2	982	10	ACC46763 Human COP
10	856.2	71.2	982	12	AD124462 Human mod
11	856.2	71.2	982	12	AD182868 Human PRO
12	663.8	55.2	2481	6	ABO88116 Human ost
13	663.8	55.2	2481	8	ABZ34778 Coding se
14	662.8	54.3	129722	6	ABO88117 Human ost
15	652.8	54.3	129722	12	AD018027 Human sof
16	522.8	43.5	3372	8	ACC46300 Human dit
17	496.4	41.3	510	10	ADK11708 Breast ca
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19	437.8	36.4	653	12	ADB77049 Human cdn
20	437.8	36.4	2066	9	ACH04136 Human cdn
21	437.8	36.4	2066	10	ADJ56457 Human cdn

22	434.2	36.1	1447	12	ADQ22623 Human sof
23	425	35.3	465	9	ACH44238 Human foe
24	423.6	35.1	429	9	ACH21548 Human adu
25	358.4	29.8	360	6	ABV78204 Human ID3
26	358.4	29.8	360	6	ABZ35780 Human ID3
27	358.4	29.8	360	6	ABX10023 Human ID3
28	358.4	29.8	360	6	ABL91745 Human pol
29	358.4	29.8	360	12	AD000370 Novel hum
30	358.4	29.8	360	12	ADN98801 Novel hum
31	354	29.4	531	12	ACH76426 Human gen
32	345.8	28.7	568	10	ABT41893 Toxicity
33	335.4	27.9	517	6	ABO39801 Oligonuc1
34	335.4	27.9	517	6	ABO39800 Oligonuc1
35	309	25.7	495	4	AA122113 Probe #12
36	309	25.7	495	4	ABA67192 Human foe
37	309	25.7	495	4	AA147408 Probe #16
38	309	25.7	495	4	ABA49278 Human bre
39	309	25.7	495	4	ABA34287 Probe #12
40	309	25.7	495	4	AAK41370 Human bon
41	309	25.7	495	4	AAK15636 Human bra
42	309	25.7	495	4	ABS40861 Human liv
43	309	25.7	495	5	AA107811 Probe #78
44	309	25.7	495	6	ABs15375 Human gen
45	306.4	25.5	446	2	AAQ44247 HEIR-1 ge

## ALIGNMENTS

RESULT 1	ABO88115	standard; CDNA, 1203 BP.
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XX	ABO88115	
XX	ABO88115	
DT	18-SEP-2002	(first entry)
XX	18-SEP-2002	
DE	Human osteoblast differentiation related cdna seq ID NO 22.	
XX	Human, osteoblast; stem cell differentiation; bone tissue deposition;	
KW	osteoporosis; osteopathic; ss.	
XX	Homo sapiens.	
OS	Homo sapiens.	
XX	WO200250301-A2.	
PN	27-JUN-2002.	
PD	18-DEC-2001; 2001WO-US048276.	
XX	18-DEC-2001; 2000US-0255882P.	
PF	24-APR-2001; 2001US-0285691P.	
XX	(GENE-) GENE LOGIC INC.	
XX	(PROC) PROCTER & GAMBLE CO.	
XX	U D, Axelrod DW, Cook US, Jaiswal N, Einstein R, Houghton A;	
PI	Mertz L;	
XX	WPI; 2002-557663/59.	
DR	Use of genes and their expression profiles associated with osteoblast	
PT	differentiation for screening modulators bone formation, for diagnosing	
PT	or treating e.g. osteoporosis, or as markers for the differentiation	
PT	process.	
XX	Claim 1; SEQ ID NO 22; 78pp + Sequence Listing; English.	
PS	The invention relates to genes and their expression profiles are used	
XX	for: (a) screening modulators of precursor stem cell differentiation into	
CC	osteoblasts, or bone tissue deposition; (b) diagnosing abnormal	
CC	deposition of bone tissue, abnormal rate of osteoblast formation or	
CC	osteoporosis; or (c) treating or monitoring treatment of the conditions	

CC cited in (b), or monitoring the progression of bone tissue deposition.  
CC Specific conditions include postmenopausal osteoporosis, glucocorticoid  
CC osteoporosis or male osteoporosis, osteopenia, osteodys trophy, drug-  
CC induced abnormalities in bone formation or bone loss, conditions that  
CC involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis),  
CC skeletal disease linked to breast cancer, mastocytosis, Fanconi syndrome,  
CC or fibrous dysplasia. The present sequence is that of an osteoblast  
CC differentiation associated cDNA marker of the invention. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pcc\_sequences

Sequence 1203 BP, 233 A, 353 C, 350 G, 267 T, 0 U, 0 Other;

Query Match 98.0%; Score 1178.4; DB 6; Length 1203;  
Best Local Similarity 99.8%; Pred. No. 1.4e-310;

Matches 1201; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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Db 1 GATCTGGGCTGCTCCAGGAAAAAGCAATTTGGAATTAATGTTTGAATGATCTT 60  
QY 61 AAATCTTGTGCGGGAGAGCCCGCTCTCCCGGATAGCGCTTCTCATTTCTTGA 120  
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Db 121 ATCCGGGCTCCCGGCTCTTCCGCGTCAAGACAGCCGAGAGAGCTGTTTGAATTTA 180  
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Db 241 GAGGCGTCCCTTCAGGAGAGCTCTAATAAGTGAACGCGCGGAGCGGCGGCTTGC 300  
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QY 421 GGAAGCAATCTGGCCATGCGCCGCGGCGAGAGAGGCGCGAGCTGAAGAGCGCT 480  
Db 421 GGAAGCAATCTGGCCATGCGCCGCGGCGAGAGAGGCGCGAGCTGAAGAGCGCT 480  
QY 481 GAGCTTGTGAGAGCATGAACCACTGCTACCTCCGCTGCGGAACTGTACCCGAGT 540  
Db 481 GAGCTTGTGAGAGCATGAACCACTGCTACCTCCGCTGCGGAACTGTACCCGAGT 540  
QY 541 CCCGAGGCACTGAGCTTGAAGCAGGTGAAATCTTAAGCGGCTCATCACTTCTT 600  
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Db 601 GAGCTGAGGTGCTGCGGCGAGCCAGCCCTGAGACCCCTGATGAGCCCACTTCC 660  
QY 661 CATCCAGACAGCCAGCTGCTCCGAGAACTTGTATCTCCAGAACTTGTATCTT 720  
Db 661 CATCCAGACAGCCAGCTGCTCCGAGAACTTGTATCTCCAGAACTTGTATCTT 720  
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Db 1141 CTTTATACAGGAG 1199  
QY 1200 AGTT 1203  
Db 1200 AGTT 1203  
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XX  
AC ADH28990;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Human chronic myelogenous leukaemia (CML) gene marker #258.  
XX  
KW de; chronic phase chronic myelogenous leukaemia; CP-CML;  
KW blast crisis CML; BC-CML; human; chronic myelogenous leukaemia;  
KW gene marker.  
XX  
OS Homo sapiens.  
XX  
PN US2003104426-A1.  
XX  
PD 05-JUN-2003.  
XX  
PF 14-JUN-2002; 2002US-00171581.  
XX  
PR 18-JUN-2001; 2001US-0298914P.  
XX  
PA (LINS/) LINSLEY P S.  
PA (MAOM/) MAO M.  
PA (DAIH/) DAI H.  
PA (HEXY/) HE Y.  
PA (RADJ/) RADICH J P.  
PI Linsley PS, Mao M, Dai H, He Y, Radich JP;  
XX  
XX WPI; 2003-787046/74.  
XX  
PT Classifying cell sample as chronic phase chronic myelogenous leukemia or  
PT blast crisis chronic myelogenous leukemia by detecting difference in  
PT expression of genes corresponding to the markers such as X15415, U89436.  
XX  
PS Disclosure; SEQ ID NO 258; 31bp; English.  
XX  
CC The invention relates to a method of classifying a cell sample as chronic  
CC phase chronic myelogenous leukaemia (CP-CML) or blast crisis CML (BC-  
CC CML). The method is useful for classifying a sample as CP-CML or BC-CML.

CC The present sequence represents a human chronic myelogenous leukaemia  
CC (CML) gene marker used to distinguish blast crisis CML from chronic phase  
CC CML.  
XX

Sequence 1203 BP, 233 A, 353 C, 350 G, 267 T, 0 U, 0 Other;

Query Match 98.0%; Score 1178.4; DB 10; Length 1203;  
Best Local Similarity 99.8%; Pred. No. 1.4e-310;  
Matches 1201; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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DB 1 GATCTGGGGTGTGCTGCAGGAAAAGCAATTCTGAAAGTTAATGTTTTGATGATTTCTT 60
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DB 61 AAATCTTGTCTGCGGAGAGGCGGCTCTTCCCGATACAGCGCTTCTCATTTCTTTGA 120
QY 121 ATCCGCGGCTCCGCGGCTTTCGAGCTCAGACGAGCGAGAAAGCGTGTTCGAAATTTAA 180
DB 121 ATCCGCGGCTCCGCGGCTTTCGAGCTCAGACGAGCGAGAAAGCGTGTTCGAAATTTAA 180
QY 181 GCGGGCTGTGAACGCCAGAGGCGCGCGGGGCGGGGCGAGGCGGGCCATTTTGAATAA 240
DB 181 GCGGGCTGTGAACGCCAGAGGCGCGCGGGGCGGGGCGAGGCGGGCCATTTTGAATAA 240
QY 241 GAGGGGTGCTTCCAGGCAAGGCTCTAATAAGTACCGCGCGCGCGCGCGCGGCTTGC 300
DB 241 GAGGGGTGCTTCCAGGCAAGGCTCTAATAAGTACCGCGCGCGCGCGCGCGGCTTGC 300
QY 301 AGGTACTGTAGCGGACTCTTTTGGTTTCTTTCTTTTGGGAGACCTCTGAGCACT 360
DB 301 AGGTACTGTAGCGGACTCTTTTGGTTTCTTTCTTTTGGGAGACCTCTGAGCACT 360
QY 361 CCCCAAGCATGAAGGCGCTAGAGCCCGGTGCGCGCTGTCTAGAGCGGTGTGCTGTCT 420
DB 361 CCCCAAGCATGAAGGCGCTAGAGCCCGGTGCGCGCTGTCTAGAGCGGTGTGCTGTCT 420
QY 421 GGAAGCGAGTCTGGCCATGCGCCGCGGCGCGAGGAAAGGCGCGGAGCTGAGAGCCGT 480
DB 421 GGAAGCGAGTCTGGCCATGCGCCGCGGCGCGAGGAAAGGCGCGGAGCTGAGAGCCGT 480
QY 481 GAGCTTGTGCGAGCATGAACCATGCTACTCCCGCTGCGGGAACGTGTATCCCGGAGT 540
DB 481 GAGCTTGTGCGAGCATGAACCATGCTACTCCCGCTGCGGGAACGTGTATCCCGGAGT 540
QY 541 CCCGAGAGGCACTAGCTTAGCCAGGTGGAATCTCTACAGCGCGTCACTGATCTTCT 600
DB 541 CCCGAGAGGCACTAGCTTAGCCAGGTGGAATCTCTACAGCGCGTCACTGATCTTCT 600
QY 601 CGAAGCTGCAAGTATGTCCTGCGGAGCGAGCCCTCTGAGACCCCTGATGCGCCACCTTTC 660
DB 601 CGAAGCTGCAAGTATGTCCTGCGGAGCGAGCCCTCTGAGACCCCTGATGCGCCACCTTTC 660
QY 661 CATTCAGAGAGCGAGCTGCTCCGGAATTTGTCAATCTCAACGACAAAGAGAGCTTTTG 720
DB 661 CATTCAGAGAGCGAGCTGCTCCGGAATTTGTCAATCTCAACGACAAAGAGAGCTTTTG 720
QY 721 CCACTGACTGCGCGCGTGTCTTGAACCTTCAGAAAGCAGAGTCTGCGCGCTTGTGCT 780
DB 721 CCACTGACTGCGCGCGTGTCTTGAACCTTCAGAAAGCAGAGTCTGCGCGCTTGTGCT 780
QY 781 GGGAGCCCGGGAACCTTCTTCCGCGAGAGCCGAGCGGAGAGTGGGCCCAACTTTCGCC 840
DB 781 GGGAGCCCGGGAACCTTCTTCCGCGAGAGCCGAGCGGAGAGTGGGCCCAACTTTCGCC 840
QY 841 CTGGCCACTTGAATCAACCAATCCCTTCTGGAAGCTAACTGCTGTGCGAGCGAA 900
DB 841 CTGGCCACTTGAATCAACCAATCCCTTCTGGAAGCTAACTGCTGTGCGAGCGAA 900
QY 901 GGAAGTGTGAATCTTGTAGCTTGAAGAGCCAGAGCTAGCTTGGCCACAGAGCTGGGAGCT 960
DB 901 GGAAGTGTGAATCTTGTAGCTTGAAGAGCCAGAGCTAGCTTGGCCACAGAGCTGGGAGCT 960
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QY 961 CACCGTGTCCACACCCACCCCAAGTCTTAAGTCTTTTCAAGAGCGTGAAGTGTGAA 1020
DB 961 CACCGTGTCCACACCCACCCCAAGTCTTAAGTCTTTTCAAGAGCGTGAAGTGTGAA 1020
QY 1021 GAGAGTGTGCTCTCCAAACTATGCGCAAGGCGCGGAGAGCTGTCTTGTGCTCTT 1080
DB 1021 GAGAGTGTGCTCTCCAAACTATGCGCAAGGCGCGGAGAGCTGTCTTGTGCTCTT 1080
QY 1081 GAGAGAGGTTCTGTGCTGCTGATTTATGAACCTATAATAG-GTATATAGTTTGTAC 1139
DB 1081 GAGAGAGGTTCTGTGCTGCTGATTTATGAACCTATAATAGAGTATATAGTTTGTAC 1140
QY 1140 CTTTTTTCAGAGAAAGTGAATTTCTGTATACAAAGCGATATATTAATCTTTTATAAA 1199
DB 1141 CTTTTTTCAGAGAAAGTGAATTTCTGTATACAAAGCGATATATTAATCTTTTATAAA 1199
QY 1200 AGTT 1203
DB 1200 AGTT 1203
```

RESULT 3  
ACH04136  
ID ACH04136 standard; cDNA; 2066 BP.

ACH04136;  
26-SEP-2003 (first entry)

Human cDNA differentially expressed in lung cancer #341.

Gene therapy; emphysema; sb; gene; chronic obstructive pulmonary disease;  
respiratory disorder; lung cancer; asthma; human.

Homo sapiens.

US2003065157-A1.

03-APR-2003.

04-APR-2002; 2002US-00116802.

04-APR-2001; 2001US-0281593P.

(LASE/) LASEK A W.

Lasek AW;

WPI; 2003-540803/51.

New combination comprising cDNAs that are differentially expressed in  
respiratory disorders, useful for diagnosing or treating respiratory  
disorders e.g., lung cancer, chronic obstructive pulmonary disease,  
emphysema or asthma.

Claim 1; Page: 39pp; English.

The invention relates to a combination comprising cDNAs or their  
complements that are differentially expressed in respiratory disorder.  
The combination is useful for preparing a composition for diagnosing or  
treating respiratory disorders e.g., lung cancer, chronic obstructive  
pulmonary disease, emphysema or asthma. The present sequence represents  
human cDNA differentially expressed during lung cancer

Sequence 2066 BP; 446 A; 564 C; 594 G; 455 T; 0 U; 7 Other;

Query Match 96.8%; Score 1164.2; DB 9; Length 2066;  
Best Local Similarity 99.5%; Pred. No. 1.3e-306;  
Matches 1199; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

```
QY 1 GATCTGGGGTGTGCTGCAGGAAAAGCAATTCTGAAAGTTAATGTTTTGATGATTTCTT 60
|||
```



QY 1 GATCTGGGTGCTGCACAGAAAAAGCAATTCGTGAAGTTAATGCTTTGAGTATCTT 60  
Db 176 GATCTGGGTGCTGCACAGAAAAAGCAATTCGTGAAGTTAATGCTTTGAGTATCTT 235  
QY 61 AATCTCTTCTGAGGAGAGCCCGCTCTCCCGGATCAGGCTCTCTCAATCTTGA 120  
Db 236 AATCTCTTCTGAGGAGAGCCCGCTCTCCCGGATCAGGCTCTCTCAATCTTGA 295  
QY 121 ATCCGCGGCTCCGCGGCTCTTCCGCGTCAAGACGAGCCGAGGAAGCTGTTTCAATTAA 180  
Db 296 ATCCGCGGCTCCGCGGCTCTTCCGCGTCAAGACGAGCCGAGGAAGCTGTTTCAATTAA 355  
QY 181 GGGGGCTGTGAACGCCAGAGCCCGGGGGGGGGGGCCAGAGCGGGCCATTTGAAATAA 240  
Db 356 GGGGGCTGTGAACGCCAGAGCCCGGGGGGGGGGGCCAGAGCGGGCCATTTGAAATAA 415  
QY 241 GAGGCGTGCCTTCCAGGCAAGGCTCTAATAAGTACCGCCGCGGAGCGTGCAGCGTGC 300  
Db 416 GAGGCGTGCCTTCCAGGCAAGGCTCTAATAAGTACCGCCGCGGAGCGTGCAGCGTGC 475  
QY 301 AGGTCACTGTAGC-GGACTTCTTTTGGTTTCTTTTCTTTTGGGAGCACTTGACTAC 359  
Db 476 AGGTCACTGTAGGAGGACTTCTTTTGGTTTCTTTTCTTTTGGGAGCACTTGACTAC 535  
QY 360 TCCCGAGCATGAAAGGCGCTGAGCCCGGCTGCGGCTGCTACAGAGGGGTGTGCTGCTGT 419  
Db 536 TCCCGAGCATGAAAGGCGCTGAGCCCGGCTGCGGCTGCTACAGAGGGGTGTGCTGCTGT 595  
QY 420 CGGAAACGAGTCTGAGCATCGCCCGGGGGCGAGGGAAGGGCCCGGAGCTGAGAGCGCG 479  
Db 596 CGGAAACGAGTCTGAGCATCGCCCGGGGGCGAGGGAAGGGCCCGGAGCTGAGAGCGCG 655  
QY 480 TGAGCTTGTGAGCAGCATGAACCACTGTACTCCCGCTGCGGGAACTGTAAACCGGAG 539  
Db 656 TGAGCTTGTGAGCAGCATGAACCACTGTACTCCCGCTGCGGGAACTGTAAACCGGAG 715  
QY 540 TCCCGAGAGCACTCAGCTTATGCGAGGTGGAATCTTACAGGCGCTCATGACTATTC 599  
Db 716 TCCCGAGAGCACTCAGCTTATGCGAGGTGGAATCTTACAGGCGCTCATGACTATTC 775  
QY 600 TGAGCTTGTGAGTATGCTGAGCGAGCGAGCCCTTGAGACCCCTGATGAGCCCACTTC 659  
Db 776 TGAGCTTGTGAGTATGCTGAGCGAGCGAGCCCTTGAGACCCCTGATGAGCCCACTTC 835  
QY 660 CCATCCAGACAGCGGAGCTCGCTCCGGAATTGTCTATCTTCAACGACAAAGAGCTTT 719  
Db 836 CCATCCAGACAGCGGAGCTCGCTCCGGAATTGTCTATCTTCAACGACAAAGAGCTTT 895  
QY 720 GCCACTGATCGGCGCGTGTCTGACACCTTCAGACAGCGAGTGTGCGCCGCTTTCGC 779  
Db 896 GCCACTGATCGGCGCGTGTCTGACACCTTCAGACAGCGAGTGTGCGCCGCTTTCGC 955  
QY 780 TGGGAGCCCGGGGAACCTCTCTGCGGGAAGCGGAGCGGAGGGAATGGGCCCAACTTGC 839  
Db 956 TGGGAGCCCGGGGAACCTCTCTGCGGGAAGCGGAGCGGAGGGAATGGGCCCAACTTGC 1015  
QY 840 CCTGCCCACTTGAATTCACCAATTCCTTCTGAGACTTAACTGTGCTCAGAGCGA 899  
Db 1016 CCTGCCCACTTGAATTCACCAATTCCTTCTGAGACTTAACTGTGCTCAGAGCGA 1075  
QY 900 AGGACTGTGAATTTGAGCTGGAAGGCGAGAGCTAGTCTGCGCACAGCTGGCGAGC 959  
Db 1076 AGGACTGTGAATTTGAGCTGGAAGGCGAGAGCTAGTCTGCGCACAGCTGGCGAGC 1135  
QY 960 TCACCTGTGCCACCCCAAGTTCTTAAGTCTTTTTCAGACGAGGAGGTGGA 1019  
Db 1136 TCACCTGTGCCACCCCAAGTTCTTAAGTCTTTTTCAGACGAGGAGGTGGA 1195  
QY 1020 AGGAGTGGTGTCTTCAAACTATGCGAAGCGCGGAGAGCTGTCTTCTGCTCTCT 1079  
Db 1196 AGGAGTGGTGTCTTCAAACTATGCGAAGCGCGGAGAGCTGTCTTCTGCTCTCT 1255

QY 1080 TGGAGAAAGTTCTGTGCCCTGATTATGACTATTAATAG-GTATATAGTTTGA 1138  
Db 1256 TGGAGAAAGTTCTGTGCCCTGATTATGACTATTAATAGTTATAGTTTGA 1315  
QY 1139 CTTTTTACAGGAGGAGTGAATTTCTGTAACATGCGATGTATTAACCTTTTAA 1198  
Db 1316 CTTTTTACAGGAGGAGTGAATTTCTGTAACATGCGATGTATTAACCTTTTAA 1374  
QY 1199 AAGTT 1203  
Db 1375 AAGTT 1379  
RESULT 5  
AAAF21652 standard; DNA; 1300 BP.  
AAAF21652;  
27-MAR-2001 (first entry)  
XX  
DE Human breast and ovarian cancer associated antigen gene SEQ ID 39.  
XX  
KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;  
KW neotropic; neuroprotective; antiviral; antiallergic; hepatotropic;  
KW antidiabetic; antineoplastic; antitumor; anticonvulsant;  
KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;  
KW Addison's disease; allergy; autoimmune haemolytic anaemia;  
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;  
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;  
KW cardiovascular disorder; wound healing; neurological disease; de.  
XX  
OS Homo sapiens.  
XX  
PN WO2005173-A1.  
XX  
PD 21-SEP-2000.  
XX  
PF 08-MAR-2000; 2000MO-US005881.  
XX  
PR 12-MAR-1999; 99US-0124270P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM;  
XX  
DR MPI; 2000-611515/58.  
XX  
DR P-PSDB; AAB58749.  
XX  
PT New human breast and ovarian cancer associated gene sequences and the  
PT polypeptides encoded by these genes, useful in the prevention, treatment  
PT and diagnosis of cancer, immune disorders, cardiovascular disorders and  
PT neurological diseases.  
XX  
PS Claim 1; Page 509-510; 1299pp; English.  
XX  
CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human  
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are  
CC associated with breast and ovarian cancer. Included in the invention are  
CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the  
CC isolation and characterisation of the DNA and protein sequences of the  
CC invention. The breast and ovarian cancer associated DNA, protein, agonist  
CC or antagonist sequences exhibit cytostatic; immunosuppressive; neotropic;  
CC neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;  
CC antineoplastic; antitumor; anticonvulsant; antidiabetic;  
CC antifungal; antiparasitic and cardiac activity. The polynucleotide and  
CC protein sequences are used in the diagnosis of cancer, particularly  
CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists  
CC and agonists may also be used in the diagnosis, prevention and treatment  
CC of immune disorders e.g. Addison's disease, allergies, autoimmune  
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's  
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;  
CC cardiovascular disorders such as myocardial ischaemia; wound healing;





PS Claim 2; SEQ ID NO 221; 591bp; English.  
XX The invention relates to novel human diagnostic and therapeutic  
CC polynucleotides designated dithp (ACC46080-ACC6749) and to their encoded  
CC proteins (DITHP; ABR4116-ABR4182). The invention also relates to  
CC polynucleotide sequences at least 90% identical to the dithp cDNA  
CC sequences of the invention; recombinant vectors, host cells and  
CC transgenic organisms comprising a dithp nucleic acid sequence; the  
CC recombinant production of DITHP proteins; antibodies specific for DITHP  
CC proteins; microarrays comprising dithp nucleic acid sequences; methods of  
CC detecting dithp nucleotide and protein sequences; methods of screening  
CC for compounds which specifically bind a DITHP protein; and methods of  
CC assessing the toxicity of test compounds using a dithp hybridisation  
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the  
CC diagnosis of a wide variety of conditions including cancer and other cell  
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,  
CC viral, fungal or parasitic infections; hormonal disorders; metabolic  
CC disorders; neurological disorders; gastrointestinal disorders; transport  
CC disorders; and connective tissue disorders. They may also be used to  
CC screen for modulators of protein activity or gene expression. DITHP  
CC proteins can additionally be used in analysis of the proteome of a tissue  
CC or cell type and to induce antibodies. The dithp nucleic acids are  
CC additionally useful in somatic or germline gene therapy of the disorders  
CC mentioned above, as a source of antisense sequences, as a source of  
CC probes and primers, in genotyping and identification of individuals, in  
CC the generation of transgenic animal models of human disease or knock in  
CC humanised animals, in toxicological testing, and in transcript imaging.  
CC The present sequence represents a dithp cDNA encoding a DITHP protein  
CC which has transcription factor activity. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 3372 BP; 723 A; 947 C; 959 G; 743 T; 0 U; 0 Other;

Query Match 72.3%; Score 870.2; DB 8; Length 3372;  
Best Local Similarity 99.3%; Pred. No. 2.2e-226;  
Matches 905; Conservative 0; Mismatches 3; Indels 3; Gaps 3;

QY 295 CGTTCAGGTCAGTGTAGC-GGACTTCTTTGTTTCTTTCTTTGGGGCACTCTGG 353  
DB 2673 CTTGGCAGGTCACTGTAGCGGAGCTTTTGTGTTTCTTTCTTTGGGGCACTCTGG 2614  
QY 354 ACTCACTCCCGAGCATGAAGGGCGTGAAGCCGCTGGCGCTGATCAAGAGGGGTGTGT 413  
DB 2613 ACTCACTCCCGAGCATGAAGGGCGTGAAGCCGCTGGCGCTGATCAAGAGGGGTGTGT 2554  
QY 414 GCCTGTGGGAAGCGAGTGTGAGCCATGCGCCGGGGCCGAGGAAGGCCCGGAGCTGAGG 473  
DB 2553 GCCTGTGGGAAGCGAGTGTGAGCCATGCGCCGGGGCCGAGGAAGGCCCGGAGCTGAGG 2494  
QY 474 AGCCGCTGAGTGTGTGAGCATGAACACTGTCTCCGCTGCGGGAACTGTATC 533  
DB 2493 AGCCGCTGAGTGTGTGAGCATGAACACTGTCTCCGCTGCGGGAACTGTATC 2434  
QY 534 CCGGAGTCCCGAGGCACTCAAGCTTAGCCAGGTGAATCTTCAAGCGCGTCACTGACT 593  
DB 2433 CCGGAGTCCCGAGGCACTCAAGCTTAGCCAGGTGAATCTTCAAGCGCGTCACTGACT 2374  
QY 594 ACATTTGAGACCTGAGGTAGTCTGAGCGAGGCAAGCCCTGGAACCCCTGATGAGCCCCC 653  
DB 2373 ACATTTGAGACCTGAGGTAGTCTGAGCGAGGCAAGCCCTGGAACCCCTGATGAGCCCCC 2314  
QY 654 ACCTTCCATCCAGACAGCCGAGCTGCTCCGAACTTGTCACTTCCAAAGCAAAAGGA 713  
DB 2313 ACCTTCCATCCAGACAGCCGAGCTGCTCCGAACTTGTCACTTCCAAAGCAAAAGGA 2254  
QY 714 GCTTTTGCACCTGACTCGGCGGTGTCTTCAACCTTCAAAAGCAGAGTCTGCGCCGCT 773  
DB 2253 GCTTTTGCACCTGACTCGGCGGTGTCTTCAACCTTCAAAAGCAGAGTCTGCGCCGCT 2194  
QY 774 TCTGCTGGGAGCCCGGAACTCTCTCTCCGGAAGCCGGAAGGAGATGGGCCCA 833

DB 2193 TCTGCTGGGAGCCCGGAACTCTCTCTCCGGAAGCCGGAAGGATGGGCCCA 2134  
QY 834 CTTGCGCCCTGCGCACTTGAATCAACCAATCCCTTCTGAGACTAAACCTGGTCTAG 893  
DB 2133 CTTGCGCCCTGCGCACTTGAATCAACCAATCCCTTCTGAGACTAAACCTGGTCTAG 2074  
QY 894 GAGCGAAGACTGTGAACCTTGTAGCTGAGAGGCAAGCAAGTACTGTGCGCACCACTGG 953  
DB 2073 GAGCGAAGACTGTGAACCTTGTAGCTGAGAGGCAAGCAAGTACTGTGCGCACCACTGG 2014  
QY 954 GCGAGTACCTGTCTGCCACCCCAACCCCAAGTTCTAAGTCTTTTCAAGAGCTGAGG 1013  
DB 2013 GCGAGTACCTGTCTGCCACCCCAACCCCAAGTTCTAAGTCTTTTCAAGAGCTGAGG 1954  
QY 1014 TGTGAAGAGTGTGTCTTCCAACTATGCCAAGGGGGGCGAGCTGTCTTCTGG 1073  
DB 1953 TGTGAAGAGTGTGTCTTCCAACTATGCCAAGGGGGGCGAGCTGTCTTCTGG 1894  
QY 1074 TCTCCTTGAGAAAGTTCTGTGCGCTGATTTATGAATCTATATAG-GTATATAGT 1132  
DB 1893 TCTCCTTGAGAAAGTTCTGTGCGCTGATTTATGAATCTATATAGAGATATAGT 1834  
QY 1133 TTTGTACCTTTTTCACAGGAAAGTGAATTTCTGTACAAATGCGATGTATATTAACCTT 1192  
DB 1833 TTTGTACCTTTTTCACAGGAAAGTGAATTTCTGTACAAATGCGATGTATATTAACCTT 1775  
QY 1193 TTTATTAAGTT 1203  
DB 1774 TTTATTAAGTT 1764

RESULT 7  
AAQ4245  
ID AAQ4245 standard; cDNA; 982 BP.  
XX  
XX AAQ4245;  
AC  
XX  
DT 25-MAR-2003 (revised)  
DT 23-NOV-1993 (first entry)  
XX  
XX HEIR-1 gene.  
DE  
XX  
XX Neuroblastoma; helix-loop-helix; allele; tumour; hepatoma; N-myc;  
KW deletion; lp36.2-p36.1; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX  
FH Key Location/Qualifiers  
FT 37..483  
FT CDS /tag= b  
FT /label= HEIR-1  
FT /note= "Claim 1; Page 48"  
FT CDS 124..483  
FT /tag= a  
FT misc\_signal 858..862  
FT /tag= d  
FT /note= "ATTTA-sequence"  
FT polyA\_signal 971..976  
FT /tag= c  
XX  
XX MO9313205-A1.  
PN  
XX  
XX 08-JUL-1993.  
PD  
XX  
XX 19-DEC-1992; 92WO-BP002962.  
PF  
XX  
XX 23-DEC-1991; 91AT-00002559.  
PR  
XX  
XX (BOEH ) BOEHRINGER INGELHEIM INT GMBH.  
PA (GETH ) GENENTECH INC.  
XX  
XX  
XX Elmeier W, Welch A;

DR WPI; 1993-227321/28.  
 DR P-PSDB; AAR38910.  
 XX  
 PT Human DNA mapped in neuroblastoma consensus deletion region for gene  
 PT regulator - comprises nucleic acid sequence encoding specific aminoacid  
 PT helix loop helix protein for antibodies, for diagnosing pathological  
 PT conditions e.g. hepatoma.  
 XX  
 PS  
 XX Disclosure; Page 41-42; 67pp; German.  
 CC The gene is situated in the region of the neuroblastoma consensus  
 CC deletion 1p36.2-p36.1 and codes for a helix-loop-helix protein with the  
 CC designation HEIR-1. The gene is affected significantly by allelic tumour  
 CC deletions in neuroblastomas and correlates inversely both with N-myc  
 CC overexpression in tumours and with N-myc expression in normal  
 CC development. The cDNA and antibodies coding for HEIR-1 are used for the  
 CC diagnosis of pathological conditions associated with aberrations in the  
 CC region of the neuroblastoma consensus deletion. (Updated on 25-MAR-2003  
 CC to correct PN field.)  
 XX  
 SQ Sequence 982 BP; 211 A; 290 C; 263 G; 218 T; 0 U; 0 Other;  
 Query Match 71.2%; Score 856.2; DB 2; Length 982;  
 Best Local Similarity 97.7%; Pred. No. 8.e-223;  
 Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;  
 QY 284 GAGCGTGGCGCGCTTGGAGGCTGATGAGCGGACTTCTTTGGTTCTTCTCTTGGG 343  
 DB 40 GATCCTGCACCGAGGAACTCAGACCTCACTTCTTTGGTTCTTCTCTTGGG 99  
 QY 344 GCACCTTGGAGATCACTCCCGAGATGAGCGCTGAGCGCGCTGCTACGAG 403  
 DB 100 GCACCTTGGAGATCACTCCCGAGATGAGCGCTGAGCGCGCTGCTACGAG 159  
 QY 404 GCGGTGTGCTGCTGTGCGAAGCAGATGCGCATGCGCGCGCGCGCGAGAGAGCGCG 463  
 DB 160 GCGGTGTGCTGCTGTGCGAAGCAGATGCGCATGCGCGCGCGCGAGAGAGCGCG 219  
 QY 464 GCAGCTGAGAGAGCGCTGAGCTTGTGAGCAGATGAGCAGTGTACTCCCGCTGGG 523  
 DB 220 GCAGCTGAGAGAGCGCTGAGCTTGTGAGCAGATGAGCAGTGTACTCCCGCTGGG 279  
 QY 524 GAACCTGTACCCGAGATCCCGAGAGCAGTCACTGAGCTTACCTCCCGCTGGG 583  
 DB 280 GAACCTGTACCCGAGATCCCGAGAGCAGTCACTGAGCTTACCTCCCGCTGGG 339  
 QY 584 GTGATGACTCAATTCGACCTGAGGTAGTCTGCGCGAGCGCGCTGAGCGCGCT 643  
 DB 340 GTGATGACTCAATTCGACCTGAGGTAGTCTGCGCGAGCGCGCTGAGCGCGCT 399  
 QY 644 GATGCGCGCGCGCTTCCCATCCAGAGCGAGCTGCTGCGGAACTTGTATCTCCAC 703  
 DB 400 GATGCGCGCGCGCTTCCCATCCAGAGCGAGCTGCTGCGGAACTTGTATCTCCAC 459  
 QY 704 GACAAAGAGAGCTTTTGCACAGTACCTGCGCGGTGCTGAGACCTCCGAGAGCGAGTGC 763  
 DB 460 GACAAAGAGAGCTTTTGCACAGTACCTGCGCGGTGCTGAGACCTCCGAGAGCGAGTGC 519  
 QY 764 TGGCGCGCGCTTGTGCTTGGAGAGCGCGGAGCTCTGCTGCGGAGCGAGCGAGGGA 823  
 DB 520 TGGCGCGCGCTTGTGCTTGGAGAGCGCGGAGCTCTGCTGCGGAGCGAGCGAGGGA 579  
 QY 824 TGGCGCGCGAGCTTGGCGCGCGCGCTTGAATTCCTTCTCTGAGACTTAAAC 883  
 DB 580 TGGCGCGCGAGCTTGGCGCGCGCGCTTGAATTCCTTCTCTGAGACTTAAAC 639  
 QY 884 TGGTCTGAGAGAGCGAGAGCTGTGAATTTGAGCTGAGAGCGAGCTAGCTGGC 943  
 DB 640 TGGTCTGAGAGAGCGAGAGCTGTGAATTTGAGCTGAGAGCGAGCTAGCTGGC 699  
 QY 944 CACGAGCTGGGCGAGCTACCTGCTCCAGCCCAACCCCAAGTTCTTAAGTCTTTTCA 1003  
 DB 700 CACGAGCTGGGCGAGCTACCTGCTCCAGCCCAACCCCAAGTTCTTAAGTCTTTTCA 758

QY 1004 AGCGTGGAGCTGTGAGAGAGTGGTCTCTCCAACTATGCCAAGCGCGGAGAGCT 1063  
 DB 759 AGCGTGGAGCTGTGAGAGAGTGGTCTCTCCAACTATGCCAAGCGCGGAGAGCT 818  
 QY 1064 GGTCTTGTGCTCTCTTGGAGAGAGTCTGTGCTCCGCTGATTTATGAACTTATATAG- 1122  
 DB 819 GGTCTTGTGCTCTCTTGGAGAGAGTCTGTGCTCCGCTGATTTATGAACTTATATAG 878  
 QY 1123 GATATAGCTTTTGTACTTTTATACAGGAGAGTGACTTGTGTAACAATGCGATAT 1182  
 DB 879 GATATAGCTTTTGTACTTTTATACAGGAGAGTGACTTGTGTAACAATGCGATAT 937  
 QY 1183 ATTAACTTTTATATAAGTT 1203  
 DB 938 ATTAACTTTTATATAAGTT 958  
 RESULT 8  
 ABQ88114  
 ID ABQ88114 standard; cDNA; 982 BP.  
 AC ABQ88114;  
 XX  
 DT 18-SEP-2002 (first entry)  
 XX  
 DE Human osteoblast differentiation related cDNA SEQ ID NO 21.  
 XX Human; osteoblast; stem cell differentiation; bone tissue deposition;  
 KW osteoporosis; osteopathic; ss.  
 XX Homo sapiens.  
 XX  
 EN W0200250301-A2.  
 PD 27-JUN-2002.  
 XX  
 PF 18-DEC-2001; 2001MO-US048276.  
 XX  
 FR 18-DEC-2000; 2000US-0255882P.  
 PR 24-APR-2001; 2001US-0285691P.  
 XX  
 PA (GENE-) GENE LOGIC INC.  
 PA (PROCTER & GAMBLE CO.  
 PI JI D, Axelrod DW, Cook JS, Jalewal N, Einstein R, Houghton A;  
 PI Mertz L;  
 DR WPI; 2002-557663/59.  
 PT Use of genes and their expression profiles associated with osteoblast  
 PT differentiation for screening modulators bone formation, for diagnosing  
 PT or treating e.g. osteoporosis, or as markers for the differentiation  
 PT process.  
 XX  
 PS Claim 1; SEQ ID NO 21; 78bp + Sequence Listing; English.  
 XX  
 CC The invention relates to genes and their expression profiles are used  
 CC for: (a) screening modulators of precursor stem cell differentiation into  
 CC osteoblasts, or bone tissue deposition; (b) diagnosing abnormal  
 CC deposition of bone tissue, abnormal rate of osteoblast formation or  
 CC osteoporosis; or (c) treating or monitoring treatment of the conditions  
 CC cited in (b), or monitoring the progression of bone tissue deposition.  
 CC Specific conditions include postmenopausal osteoporosis, glucocorticoid  
 CC osteoporosis or male osteoporosis, osteopenia, osteodystrophy, drug-  
 CC induced abnormalities in bone formation or bone loss, conditions that  
 CC involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis),  
 CC or fibrous dysplasia. The present sequence is that of an osteoblast  
 CC differentiation associated cDNA marker of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 982 BP; 211 A; 290 C; 263 G; 218 T; 0 U; 0 Other;  
 SQ

Query Match 71.2%; Score 856.2; DB 6; Length 982;  
 Best Local Similarity 97.7%; Pred. No. 8.6e-223;  
 Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

284 GAGCGGCGCGGTTGACAGTCACTGATGCGGACTTCTTTGTTTCTTTCTTTGGG 343  
 DB 40 GATCTTGACACGAGGAACTCAGACACTTCTTTGTTTCTTTCTTTGGG 99  
 QY 344 GCACCTTGAGTCACTCCCGACATGAAGCGCTGAGCGCGGCTGTACGAG 403  
 DB 100 GCACTCTGAGTCACTCCCGACATGAAGCGCTGAGCGCGGCTGTACGAG 159  
 QY 404 GCGGTGTGCTGCTGTGGAAGCAGTCTGCGCATGCGCGGCGCGGAGGAGCGCG 463  
 DB 160 GCGGTGTGCTGCTGTGGAAGCAGTCTGCGCATGCGCGGCGCGGAGGAGCGCG 219  
 QY 464 GCAGCTGAGAGCGCGCTGAGCTTGTGAGCAGATGAACACTGCTACCTCCGCTGCGG 523  
 DB 220 GCAGCTGAGAGCGCGCTGAGCTTGTGAGCAGATGAACACTGCTACCTCCGCTGCGG 279  
 QY 524 GAACCTGTACCCGAGAGTCCCGAGAGGCACTCAGCTTACGCGAGTGAATCTTACAGCG 583  
 DB 280 GAACCTGTACCCGAGAGTCCCGAGAGGCACTCAGCTTACGCGAGTGAATCTTACAGCG 339  
 QY 584 GTATGATGACTATCTGCACTGCAAGTATCTTGGCGGACGAGCCCTGAGACCCCT 643  
 DB 340 GTATGATGACTATCTGCACTGCAAGTATCTTGGCGGACGAGCCCTGAGACCCCT 399  
 QY 644 GATGCGCCCGACCTTCCATTCAGACAGCGGAGCTGCGTCCGGAATCTTGTATCTCCAC 703  
 DB 400 GATGCGCCCGACCTTCCATTCAGACAGCGGAGCTGCGTCCGGAATCTTGTATCTCCAC 459  
 QY 704 GACAAAGAGAGCTTTGACATGACTGCGCGCTGTCTTACACCTTCCAGAAAGCAGTGC 763  
 DB 460 GACAAAGAGAGCTTTGACATGACTGCGCGCTGTCTTACACCTTCCAGAAAGCAGTGC 519  
 QY 764 TGGCGCCGCTTGTGCTGGAACCCCGGAACTTCTTCCGGAAGCCGAGCGGAGGA 823  
 DB 520 TGGCGCCGCTTGTGCTGGAACCCCGGAACTTCTTCCGGAAGCCGAGCGGAGGA 579  
 QY 824 TGGCGCCCAACTTCCGCGCTGCGCACTTGAATCCCTTCTTGAAGTCTTAAAC 883  
 DB 580 TGGCGCCCAACTTCCGCGCTGCGCACTTGAATCCCTTCTTGAAGTCTTAAAC 639  
 QY 884 TGGTCTCAGAGCGAAGGACTGTGAATCTTGAAGCTGAAAGCAGAGCTAGCTTGGC 943  
 DB 640 TGGTCTCAGAGCGAAGGACTGTGAATCTTGAAGCTGAAAGCAGAGCTAGCTTGGC 699  
 QY 944 CACGAGCTGAGGAGCTCACTCTGCTCCACCCCACTTCTTGAAGTCTTCTTTCAG 1003  
 DB 700 CACGAGCTGAGGAGCTCACTCTGCTCCACCCCACTTCTTGAAGTCTTCTTTCAG 758  
 QY 1004 AGCGTGAAGTGTGAAGAGTGGCTGCTTCCAAACTTATGCGCAAGCGCGCGAGAGT 1063  
 DB 759 AGCGTGAAGTGTGAAGAGTGGCTGCTTCCAAACTTATGCGCAAGCGCGCGAGAGT 818  
 QY 1064 GGTCTTGTGCTCTCTTGAAGAAAGTCTTGTGCGCTGATTTATGAATCTTATATAG- 1122  
 DB 819 GGTCTTGTGCTCTCTTGAAGAAAGTCTTGTGCGCTGATTTATGAATCTTATATAG 878  
 QY 1123 GTATATAGTGTGTGATCTTTTATACAGGAAGTGTATCTTGTATACATGATGAT 1182  
 DB 879 GTATATAGTGTGTGATCTTTTATACAGGAAGTGTATCTTGTATACATGATGAT 937  
 QY 1183 ATTAAGTGTGTATATATATAT 1203  
 DB 938 ATTAAGTGTGTATATATATAT 958

RESULT 9

ACC46763  
 ID ACC46763 standard; cDNA; 982 BP.  
 XX  
 AC ACC46763;  
 XX  
 DT 05-JUN-2003 (first entry)  
 XX

Human COPD related protein encoding cDNA SEQ ID NO:14.

Human; chronic obstructive pulmonary disease; COPD; chronic lung disease;  
 gene; ss.

Homo sapiens.

WO200297127-A2.

05-DEC-2002.

28-MAY-2002; 2002MO-EP005835.

31-MAY-2001; 2001GB-00013266.

(FARB ) BAYER AG.

Oellers N, Gehrmann M, Kallabis H, Hall R, Schulze T, Kroegel C;

WPI; 2003-140492/13.

P-PSDB; ABP96792.

Predicting, diagnosing or prognosing chronic lung disease, by detecting a  
 chronic obstructive pulmonary disease (COPD) gene in a biological sample.

Claim 8; Page 96-97; 214pp; English.

The present invention describes a method for predicting, diagnosing or  
 prognosing chronic lung disease by detecting a chronic obstructive  
 pulmonary disease (COPD) gene related polynucleotide (see ACC46750 to  
 ACC46777, which encode the COPD related proteins in ABP96779 to  
 CC ABP96806). The method is useful for predicting, diagnosing or prognosing  
 chronic lung disease in a biological sample. The COPD genes and proteins  
 encoded by them from the present invention (I) can be used for treating  
 or preventing chronic lung disease in a mammal. (i) can be used in an  
 animal model for determining the efficacy, toxicity, or side effects of  
 treatment with (I), and determining the mechanism of action of (I).  
 CC ACC46778 to ACC46903 represent COPD related PCR primers and probes used  
 in an example from the present invention  
 CC  
 XX

Sequence 982 BP; 211 A; 290 C; 263 G; 218 T; 0 U; 0 Other;

Query Match 71.2%; Score 856.2; DB 10; Length 982;  
 Best Local Similarity 97.7%; Pred. No. 8.6e-223;  
 Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

284 GAGCGTGGCGGTTGACAGTCACTGATGCGGACTTCTTTGTTTCTTTCTTTGGG 343  
 DB 40 GATCTTGACACGAGGAACTCAGACACTTCTTTGTTTCTTTCTTTGGG 99  
 QY 344 GCACCTTGAGTCACTCCCGACATGAAGCGCTGAGCGCGGCTGTACGAG 403  
 DB 100 GCACTCTGAGTCACTCCCGACATGAAGCGCTGAGCGCGGCTGTACGAG 159  
 QY 404 GCGGTGTGCTGCTGTGGAAGCAGTCTGCGCATGCGCGGCGCGGAGGAGGCGCG 463  
 DB 160 GCGGTGTGCTGCTGTGGAAGCAGTCTGCGCATGCGCGGCGCGGAGGAGGCGCG 219  
 QY 464 GCAGCTGAGAGCGCGCTGAGCTTGTGAGCAGATGAACACTGCTACCTCCGCTGCGG 523  
 DB 220 GCAGCTGAGAGCGCGCTGAGCTTGTGAGCAGATGAACACTGCTACCTCCGCTGCGG 279  
 QY 524 GAACCTGTACCCGAGAGTCCCGAGAGGCACTCAGCTTACGCGAGTGAATCTTACAGCG 583  
 DB 280 GAACCTGTACCCGAGAGTCCCGAGAGGCACTCAGCTTACGCGAGTGAATCTTACAGCG 339

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QY 584 GTGATGAGTACATCTTGAGCTGAGAGTACGCTGGCCGAGGCCACCCCTGAGACCCCT 643
DB 340 GTGATGAGTACATCTTGAGCTGAGAGTACGCTGGCCGAGGCCACCCCTGAGACCCCT 399
QY 644 GATGGCCCCACCTTCCCATCCAGACAGCCGAGCTGCTCCGGAACCTTGTATCTCCAC 703
DB 400 GATGGCCCCACCTTCCCATCCAGACAGCCGAGCTGCTCCGGAACCTTGTATCTCCAC 459
QY 704 GACAAAAGAGCTTTTGGCACTGAGCTGGCCGCTGTCTGACACCTCCAGAACGAGGTGC 763
DB 460 GACAAAAGAGCTTTTGGCACTGAGCTGGCCGCTGTCTGACACCTCCAGAACGAGGTGC 519
QY 764 TGGCCCCGCTTCTGCTGAGGACCCCGGAGAACCTCTGCTGCGGAGGCGGACGAGGGA 823
DB 520 TGGCCCCGCTTCTGCTGAGGACCCCGGAGAACCTCTCTGCGGAGGCGGACGAGGGA 579
QY 824 TGGCCCCCACTTGGCCCTGCGCCACTTGACTTCAACAATCCCTTCTGAGACTAAACC 883
DB 580 TGGCCCCCACTTGGCCCTGCGCCACTTGACTTCAACAATCCCTTCTGAGACTGAACC 639
QY 884 TGGTGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 943
DB 640 TGGTGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 699
QY 944 CACCAAGCTGGGCGGAGCTGACCTGCTGCCAACCCCGCCAGAGTTCTAAGTCTTTTCA 1003
DB 700 CACCAAGCTGGGCGGAGCTGACCTGCTGCCAACCCCGCCAGAGTTCTAAGTCTTTTCA 758
QY 1004 AGCGTGAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1063
DB 759 AGCGTGAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 818
QY 1064 GGTCTTGTGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1122
DB 819 GGTCTTGTGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 878
QY 1123 GTATATGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1182
DB 879 GTATATGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 937
QY 1183 ATTAAACTTTTATTAAGTT 1203
DB 938 ATTAAACTTTTATTAAGTT 958

RESULT 10
AD124462
ID AD124462 standard; cDNA, 982 BP.
AC AD124462;
XX
XX 15-APR-2004 (first entry)
DT
XX
XX Human modifier of Chk1 (MCHK) encoding cDNA SEQ ID NO:12.
KW Chk1 pathway; modulating agent; modifier of Chk1; MCHK; cytoskeletal;
XX gene therapy; cancer; human; gene; ss.
XX
OS Homo sapiens.
XX
XX MO2004004785-A1.
XX
XX 15-JAN-2004.
XX
XX 09-JUL-2003; 2003WO-US021379.
XX
XX 10-JUL-2002; 2002US-0394845P.
XX
XX 16-SEP-2002; 2002US-0410986P.
XX
XX (EXEL-) EXELIXIS INC.
XX
XX Francisc-Lang H, Roche S, Joo DM, Nicoll M, Hai B, Zhang H;
PI Lickteig K, Amundsen CD, Jin Y, Adamkewicz JT, Platt DM;

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PI Hammonds RG;
XX
XX MPI: 2004-083465/08.
DR P-PSDB; AD124512.
XX
XX
PT Identifying a candidate Chk1 pathway modulating agent for treating e.g.,
PT cancer, comprises contacting an assay system comprising a MCHK
PT polypeptide or nucleic acid with a test agent and detecting a test agent-
XX biased activity.
XX
PS Example; SEQ ID NO 12; 266pp; English.
XX
XX The present invention describes a method for identifying a candidate Chk1
CC pathway modulating agent. The method comprises: (a) providing an assay
CC system comprising a modifier of Chk1 (MCHK) polypeptide or nucleic acid;
CC (b) contacting the system with a test agent, where the system provides a
CC reference activity except in the presence of the test agent; and (c)
CC detecting a test agent-biased activity, and a difference between the test
CC agent-biased activity and the reference activity. Also described: (1) a
CC method for modulating Chk1 pathway of a cell; (2) a method for modulating
CC Chk1 pathway in a mammalian cell; and (3) a method for diagnosing a
CC disease in a patient. A MCHK sequence has cytoskeletal activity, and can be
CC used in gene therapy. The method is useful for identifying a candidate
CC Chk1 pathway-modulating agent for preparing a composition for diagnosing
CC or treating e.g., cancer. The present sequence encodes a human MCHK
CC protein, which is used in the exemplification of the present invention.
XX
SQ Sequence 982 BP; 211 A; 290 C; 263 G; 218 T; 0 U; 0 Other;

Query Match 71.2%; Score 856.2; DB 12; Length 982;
Best Local Similarity 97.7%; Pred. No. 8.6e-223;
Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

QY 284 GAGGTGCGCGCGCTGACAGTCACTGAGCGGACTTTTGGTTCTTCTTTGGG 343
DB 40 GATCTGAGACCAAGGAACTCAACAGCAGCAGCTTCTTTGGG 99
QY 344 GCACCTTGGAGTCACTCCCGAGCATGAAGGCGTGAAGCCGCGTGTCTACAG 403
DB 100 GCACCTTGGAGTCACTCCCGAGCATGAAGGCGTGAAGCCGCGTGTCTACAG 159
QY 404 GCGGTGTGCTGCTGTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 463
DB 160 GCGGTGTGCTGCTGTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 219
QY 464 GCAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 523
DB 220 GCAGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 279
QY 524 GAACTGTGACCCGAGAGTCCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 583
DB 280 GAACTGTGACCCGAGAGTCCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 339
QY 584 GTGATGAGTACATCTTGAGCTGAGAGTACGCTGGCCGAGGCCACCCCTGAGACCCCT 643
DB 340 GTGATGAGTACATCTTGAGCTGAGAGTACGCTGGCCGAGGCCACCCCTGAGACCCCT 399
QY 644 GATGGCCCCACCTTCCCATCCAGACAGCCGAGCTGCTCCGGAACCTTGTATCTCCAC 703
DB 400 GATGGCCCCACCTTCCCATCCAGACAGCCGAGCTGCTCCGGAACCTTGTATCTCCAC 459
QY 704 GACAAAAGAGCTTTTGGCACTGAGCTGGCCGCTGTCTGACACCTCCAGAACGAGGTGC 763
DB 460 GACAAAAGAGCTTTTGGCACTGAGCTGGCCGCTGTCTGACACCTCCAGAACGAGGTGC 519
QY 764 TGGCCCCGCTTCTGCTGAGGACCCCGGAGAACCTCTGCTGCGGAGGCGGACGAGGGA 823
DB 520 TGGCCCCGCTTCTGCTGAGGACCCCGGAGAACCTCTCTGCGGAGGCGGACGAGGGA 579
QY 824 TGGCCCCCACTTGGCCCTGCGCCACTTGACTTCAACAATCCCTTCTGAGACTAAACC 883
DB 580 TGGCCCCCACTTGGCCCTGCGCCACTTGACTTCAACAATCCCTTCTGAGACTGAACC 639

```

[illegible]

## RESULT 11

ID	ADL82868	standard; cDNA; 982 BP.
XX		
AC	ADL82868;	
XX		
DT	17-JUN-2004	(first entry)
XX		
DE	Human PRO37957 cDNA, SEQ ID 70.	
XX		
KW	Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic;	
KW	Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory;	
KW	Gene Therapy; PRO; B cell related disorder; cancer;	
KW	immune-mediated inflammatory disease; human; gene; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2004024097-A2.	
XX		
PD	25-MAR-2004.	
XX		
PF	15-SEP-2003; 2003WO-USO29097.	
XX		
PR	16-SEP-2002; 2002US-0411392P.	
XX		
PA	(GETH ) GENENTECH INC.	
XX		
PI	Chiu H, Clark H, Dennis K, Fong S, Schoenfeld JR, Wood WI;	
PI	Wu TD;	
XX		
DR	WPI; 2004-329389/30.	
XX	P-PsDB; ADL82869.	
XX		
PT	New PRO polypeptide, useful for diagnosing and treating a B cell related	
PT	disorder, e.g. Burkitt's lymphoma, rheumatoid arthritis, autoimmune	
PT	mediated hemolytic anemia, myasthenia gravis or ankylosing spondylitis.	
PS	Claim 2; Fig 70; 695pp; English.	
XX		
XX		
CC	The present invention relates to PRO proteins and their coding sequences	
CC	The PRO proteins are useful for diagnosing and treating a B cell related	
CC	disorder, e.g. X-linked infantile hypogammaglobulinemia, polysaccharide	
CC	antigen unresponsiveness, selective IGA deficiency, selective IGM	
CC	deficiency, selective deficiency of Igg subclasses, immunodeficiency with	
CC	hyper IgM, transient hypogammaglobulinemia of infancy, Burkitt's	
CC	lymphoma, intermediate lymphoma, follicular lymphoma, type II	
CC	hypernatremia, rheumatoid arthritis, autoimmune mediated haemolytic	
CC	anemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or	
CC		

CC ankylosing spondylitis. The PRO proteins are also useful for preparing a  
CC measurement for treating a condition that is responsive to the PRO  
CC protein, e.g. cancer or immune-mediated inflammatory disease. The PRO  
CC coding sequences are useful as hybridization probes in chromosome and  
CC gene mapping, in preparing PRO proteins, or in generating transgenic  
CC animals or knockout animals, which in turn are useful in the development  
CC and screening of therapeutically useful reagents.

Sequence 982 BP; 211 A; 290 C; 263 G; 218 T; 0 U; 0 Other;

Query Match 71.2%; Score 856.2; DB 12; Length 982;

Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3

284 GAGCGTGGCGCGTTGCAAGTCACTGTAGCGACTTCTTTGGTTTCTTCTCTTTGGG 343

Db 40 GATCCTGCACCAAGGAACTCACAGCACCTCACTTCTTTGGTTTCTCTTTGGG 99

344 GCACTCTGGACTCACTCCCAAGCATGAGGCGCTGAGCCCGGTGCGCGCTGCTACGAG 403

Db 100 GCACCTCTGACTCACTCCCCAGCATGAAGGCGCTGAGCCCGGTGCCGCTGCTACGAG 159

404 GCGGTGCTGCCTGTGGAACGCACTCTGGCCATCGCCCGGGGCCGAGGGAAGGCCCG 463

Db 160 GCGGTGTCTGCCCTGTCCGAACGCACTCTGGCCATCGCCCGGGCCGAGGGAAGGCCCG 219

464 GCAGCTGAGAGCCGCTGAGCTTGCTGGACGACATGAACCACTGCTACTCCGCGCTGCGG 523

Db 220 GCAGCTGAGAGCCGCTGAGCTTGCTGGACGACATGACCACTGCTACTCCGCGCTGCGG 279

524 GAACTGGTACCCGGAGTCCCGAGAGGCACCTCAGCTTAGCCAGGTGGAATCCTACAGCGC 583

Db 280 GAACTGTTACCCGGAGTCCCGAGAGGCACCTCAGCTTAGCCAGGTGGAATCCTACAGCGC 339

584 GTCATCGACTACATTTCTCGACCTGCAGTAGTCTTGCGCGAGCCAGCCCTTGACCCCT 643

Db 340 GTCATCGACTACATTCTCGACCTGCAGTAGTCCCTGGCCGAGCCAGCCCCCTGGAACCCCT 399

644 GATGGCCCCCACCCTTCCCATCCAGACAGCCGAGCTGCTCCGGACTTGTCAATCTCCAC 703

Db 400 GATGGCCCCACCTTCCCATCCAGACAGCCGAGCTCGCTCCGAACTTGTCAATCTCCAAC 459

Qy 704 GACAAAGGAGCTTTGGCACTGACTCGGCCGTCTCTGACACCTCCAGAAGCAGGTGC 763

Db 460 GACAAAGGAGCTTTTGCCACTGACTCGGCCGTGTCCTGACACCTCCAGAACGCGAGTGC 519

Qy 764 TGGCGCCGTTCTGCTGGACCCCGGAACCTCTCTGCGGAAGCCGGACGGCAGGA 823

Db 520 TGGCGCCCGTTCCTGGGACCCCGGAACTCTCCTGCCGGAAGCCGGACGGCAGGA 579

824 TGGGCCCACTTCGCCCTGGCCCACTTGACTTCACCAATCCCTTCCTGGAGACTAAACC 883

Db 580 TGGGCCCACTTCGCCCTGCCCACTTGACTTCACCAATCCCTTCCTGGAGACTGAACC 639

884 TGGTCTCAGAGCGAAGACTGTGAACCTGTAGCCTGAGAGCCAGAGCTAGCTCTGC 943

Db 640 TGGTCTCAGGAGCGAAGGACTGTGAACCTGTGGCCTGAAGAGCCAGAGCTAGCTCTGGC 699

944 CACCAGCTGGGCGACGTCAACCTGCTCCCAACCCCAACCCCAAGTTCTAAGTCTTTTCAG 1000

Db 700 CACCAGCTGGGCGACGTCACCCCTGCTCCCAACCCCA-CCCCAAGTTCTAAGGCTTTTCAG 758

1004 AGCGTGAGGTGTGGAAGGAGTGGCTGCTCTCCAACTATGCCAAGGCGGCGCAGAGCT 106.

Db 759 AGCGTGAGGTGTGGAAGGAGTGGCTGCTCTCCAACTATGCCAAGGCGGCGCAGAGCT 818

QY 1064 GGTCTTCTGGTCTCCCTTGAGAGAAGTTCGTGCCCCGTGATTTATGAAGCTCTATATAG- 1122

Db 819 GGTCTTCTGGTCTCCTTGAGAGAAGTTCGTGTGCCCTGATTATGAAGTCTATAATAGA 878

QY 1123 G T A T A G G T T T T G T A C C T T T T T T A C A G G A G T G A C T T T C T G T A C A A T G C G A T G T A T 1183

Db 879 GATATAGGTTTGTACCTTTTACA-GGAAGTGACTTCTGTACACATGGATGTAT 937



DR WPI; 2003-058567/05.

XX Novel isolated nucleic acid upregulated/downregulated in osteogenesis,  
PT useful for bone disease therapy in subject.

XX Claim 26; Page 151; 237pp; English.

XX The present invention relates to novel nucleotide sequences, which are  
CC differentially expressed in models of osteogenesis upon being put in  
CC contact with a stimulator of osteogenesis. The present sequence is one  
CC such sequence. This sequence can be used for diagnosing osteoporosis/bone  
CC disease in a patient, promoting osteogenesis and/or preventing  
CC osteoporosis/bone disease. The present sequence encodes a transcription  
CC factor or an orphan nuclear receptor

XX Sequence 2481 BP; 521 A; 662 C; 699 G; 599 T; 0 U; 0 Other;

Query Match 55.2%; Score 663.8; DB 8; Length 2481;  
Best Local Similarity 99.7%; Pred. No. 3.5e-170;  
Matches 665; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY 1 GATCTGGGGTCTGCTCCAGAGAAAGCAATTCTGAAAGTTAATGTTTGAATGATTTCTT 60
DB 372 GATCTGGGGTCTGCTCCAGAGAAAGCAATTCTGAAAGTTAATGTTTGAATGATTTCTT 431
QY 61 AAATCTTCTGCTGGCGAGAGAGCGCCGCTTCCCGCGATACAGCGCTTCTCATTTCTTGA 120
DB 432 AAATCTTCTGCTGGCGAGAGAGCGCCGCTTCCCGCGATACAGCGCTTCTCATTTCTTGA 491
QY 121 ATCCGCGGCTCCGCGGATCTTCCGCGCTCAGACACGCGGAGAGAGCTGTTTGCATTTAA 180
DB 432 ATCCGCGGCTCCGCGGATCTTCCGCGCTCAGACACGCGGAGAGAGCTGTTTGCATTTAA 551
QY 181 GCGGGCTGTGAACGCCAGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
DB 552 GCGGGCTGTGAACGCCAGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 611
QY 241 GAGGCTGCTCTTCCAGAGAGGCTCTAATAGTACACCGCGCGGCGGCGGCGGCGGCGGCT 300
DB 612 GAGGCTGCTCTTCCAGAGAGGCTCTAATAGTACACCGCGCGGCGGCGGCGGCGGCGGCT 671
QY 301 AGGTACTGTAGCGGACCTCTTTGTTTCTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 360
DB 672 AGGTACTGTAGCGGACCTCTTTGTTTCTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 731
QY 351 CCCGAGCATGAAGGCGCTGAGCCCGGCTGCGCGGCTGCTAAGAGCGGCTGCTGCTGCT 420
DB 732 CCCGAGCATGAAGGCGCTGAGCCCGGCTGCGCGGCTGCTAAGAGCGGCTGCTGCTGCT 791
QY 421 GGAAGCGAGTCTGGCGATCGCCCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
DB 792 GGAAGCGAGTCTGGCGATCGCCCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 851
QY 481 GAGCTTGTGAGCGACATGAACCATGCTACTCCGCGCTGGGGAATGCTGCTCCGGAAGT 540
DB 852 GAGCTTGTGAGCGACATGAACCATGCTACTCCGCGCTGGGGAATGCTGCTCCGGAAGT 911
QY 541 CCCGAGGAGCACTGAGTTAGCCAGAGTGAATCTTACAGCGCGTATGATGATGATTTCT 600
DB 912 CCCGAGGAGCACTGAGTTAGCCAGAGTGAATCTTACAGCGCGTATGATGATGATTTCT 971
QY 601 GCACTGCAAGTATGCTGCGGAGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 660
DB 972 GCACTGCAAGTATGCTGCGGAGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 1031
QY 661 CATCCAG 667
DB 1032 CATCCAG 1038
```

RESULT 14  
AB088117/c  
ID AB088117 standard; cDNA; 129722 BP.

XX AB088117;

XX 18-SEP-2002 (first entry)

XX Human osteoblast differentiation related cDNA SEQ ID NO 24.

XX Human; osteoblast; stem cell differentiation; bone tissue deposition;  
XX osteoporosis; osteopathic; ss.

XX Home sapiens.

XX WO200250301-A2.

XX 27-UN-2002.

XX 18-DEC-2001; 2001WO-US048276.

XX 18-DEC-2000; 2000US-0255882P.

XX 24-APR-2001; 2001US-0285691P.

XX (GENE-) GENE LOGIC INC.

XX (PROC) PROCTER & GAMBLE CO.

XX Ji D, Axelrod DW, Cook JS, Jaiswal N, Binstein R, Houghton A;  
XX Meitz L;  
XX WPI; 2002-557663/59.

XX Use of genes and their expression profiles associated with osteoblast  
XX differentiation for screening modulators bone formation, for diagnosing  
XX or treating e.g. osteoporosis, or as markers for the differentiation  
XX process.

XX Claim 1; SEQ ID NO 24; 78pp + Sequence Listing; English.

XX The invention relates to genes and their expression profiles are used  
XX for: (a) screening modulators of precursor stem cell differentiation into  
XX osteoblasts, or bone tissue deposition; (b) diagnosing abnormal  
XX osteoblasts, or bone tissue deposition; (c) diagnosing abnormal  
XX osteoporosis; or (d) treating or monitoring treatment of the conditions  
XX cited in (b), or monitoring the progression of bone tissue deposition.  
XX Specific conditions include postmenopausal osteoporosis, glucocorticoid  
XX osteoporosis or male osteoporosis, osteopenia, osteodystrophy, drug  
XX induced abnormalities in bone formation or bone loss, conditions that  
XX involve altered bone metabolism (e.g. idiopathic juvenile osteoporosis),  
XX skeletal disease linked to breast cancer, mastocytosis, Fanconi syndrome  
XX or fibrous dysplasia. The present sequence is that of an osteoblast  
XX differentiation associated cDNA marker of the invention. Note: The  
XX sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 129722 BP; 33298 A; 32697 C; 31415 G; 32312 T; 0 U; 0 Other;

Query Match 54.3%; Score 652.8; DB 6; Length 129722;  
Best Local Similarity 99.6%; Pred. No. 1.7e-166;  
Matches 665; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

```
QY 1 GATCTGGGGTCTGCTCCAGAGAAAGCAATTCTGAAAGTTAATGTTTGAATGATTTCTT 60
DB 109558 GATCTGGGGTCTGCTCCAGAGAAAGCAATTCTGAAAGTTAATGTTTGAATGATTTT 109499
QY 61 AAATCTTCTGCTGGCGAGAGAGCGCCGCTTCCCGCGATACAGCGCTTCTCATTTCTTGA 120
DB 109498 AAATCTTCTGCTGGCGAGAGAGCGCCGCTTCCCGCGATACAGCGCTTCTCATTTCTTGA 109439
QY 121 ATCCGCGGCTCCGCGGATCTTGGCGCTCAGACACGCGGAGAGAGCTGTTTGCATTTAA 180
DB 109438 ATCCGCGGCTCCGCGGATCTTGGCGCTCAGACACGCGGAGAGAGCTGTTTGCATTTAA 109379
QY 181 GCGGGCTGTGAACGCCAGAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 18, 2004, 15:14:56 ; Search time 119.791 Seconds  
(without alignments)  
7138.064 Million cell updates/sec

Title: US-09-996-529A-5

Perfect score: 1203  
Sequence: 1 gatcgggggtctgcgcagga.....ttaacttttataaagtt 1203

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

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- 2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq:\*
- 4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq:\*
- 5: /cgn2\_6/prodata/1/ina/ECTUS\_COMB.seq:\*
- 6: /cgn2\_6/prodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	856.2	71.2	982	1	US-08-256-077-1 Sequence 1, Appli
2	856.2	71.2	982	1	US-08-466-127-1 Sequence 1, Appli
3	437.8	36.4	653	4	US-09-919-039-214 Sequence 214, App
4	360	29.9	360	1	US-08-256-077-3 Sequence 3, Appli
5	360	29.9	360	1	US-08-466-127-3 Sequence 3, Appli
6	306.4	25.5	446	1	US-08-256-077-5 Sequence 5, Appli
7	306.4	25.5	446	1	US-08-466-127-5 Sequence 5, Appli
8	198.4	16.5	255	4	US-09-513-999C-23008 Sequence 23008, A
9	75	6.2	926	1	US-08-151-391A-3 Sequence 3, Appli
10	75	6.2	926	3	US-09-561-497-3 Sequence 3, Appli
11	73.4	6.1	509	1	US-08-151-391A-1 Sequence 1, Appli
12	70	5.8	4793	3	US-09-561-497-10 Sequence 10, Appli
13	69	5.7	721	3	US-08-896-164-30 Sequence 30, Appli
14	62.8	5.2	626	4	US-09-621-976-2005 Sequence 2005, Ap
15	47.6	4.0	1309	3	US-08-362-495-4 Sequence 4, Appli
16	47.6	4.0	1309	3	US-09-408-508-4 Sequence 4, Appli
17	43.6	3.6	1635	3	US-09-234-332-4 Sequence 4, Appli
18	43.6	3.6	1635	3	US-09-702-705-1798 Sequence 1798, Ap
19	43.6	3.6	1635	4	US-09-736-457-1798 Sequence 1798, Ap
20	43.6	3.6	1635	4	US-09-671-325-1798 Sequence 1798, Ap
21	42	3.5	2175	4	US-09-252-991A-15144 Sequence 15144, A
22	42	3.5	2721	4	US-09-252-991A-14887 Sequence 14887, A
23	42	3.5	2781	4	US-09-252-991A-14482 Sequence 14482, A
24	41.8	3.5	846	4	US-09-252-991A-13245 Sequence 13245, A
25	41.8	3.5	879	4	US-09-252-991A-12714 Sequence 12714, A
26	41.8	3.5	1428	4	US-09-252-991A-12923 Sequence 12923, A
27	41.8	3.5	1455	4	US-09-252-991A-12561 Sequence 12561, A

28	40.6	3.4	703	4	US-09-799-451-19 Sequence 19, Appli
29	40.6	3.4	1287	4	US-09-799-451-469 Sequence 469, App
30	40.2	3.3	411	4	US-09-252-991A-14903 Sequence 14903, A
31	40.2	3.3	821	2	US-08-939-002A-15 Sequence 15, Appli
32	40.2	3.3	1436	3	US-09-199-637A-131 Sequence 131, App
33	40.2	3.3	3157	2	US-08-939-002A-1 Sequence 1, Appli
34	39.6	3.3	1191	4	US-09-489-039A-5044 Sequence 5044, Ap
35	39.4	3.3	1572	4	US-09-252-991A-16430 Sequence 16430, A
36	39.4	3.3	1752	4	US-09-252-991A-16164 Sequence 16164, A
37	39	3.2	1248	4	US-09-724-797-23 Sequence 23, Appli
38	39	3.2	3348	4	US-09-799-451-302 Sequence 302, App
39	39	3.2	3511	4	US-09-799-451-456 Sequence 456, App
40	38.4	3.2	1245	4	US-09-252-991A-5535 Sequence 5535, Ap
41	38.2	3.2	543	4	US-09-252-991A-8896 Sequence 8896, Ap
42	38.2	3.2	1608	4	US-09-252-991A-8091 Sequence 8091, Ap
43	38.2	3.2	1710	4	US-09-252-991A-9011 Sequence 9011, Ap
44	38.2	3.2	1920	4	US-09-252-991A-8999 Sequence 8999, Ap
45	37.6	3.1	277	2	US-08-690-011A-30 Sequence 30, Appli

ALIGNMENTS

RESULT 1  
US-08-256-077-1  
Sequence 1, Application US/08256077  
Patent No. 5654188  
GENERAL INFORMATION:  
APPLICANT: Elmeier, Wilfried  
APPLICANT: Melth, Andreas  
TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/256,077  
FILING DATE: 23-JUNE-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bemd, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 0652.1360000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 982 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-256-077-1  
Query Match  
Best Local Similarity 97.7%; Score 856.2; DB 1; Length 982;  
Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;  
QY 284 GAGCGTGGCGGGTGGACGAGTCTGTTGGTTTCTTTCTTTGGG 343  
DB 40 GATCTCGACGCCGGAACCTCAGCAGCCTTCTTTGGTTTCTTTGGG 99  
QY 344 GCACCTCTGAGACTCACTCCACGATGAAGCGCTGAGCCGCTGCTGACGAG 403

Db 100 GCACCTCTGAGTCACTCCCGGAGATGAAAGGCGCTGAGCCGGGCTGGCTGTAAG 159  
Qy 404 GCGGTGTGCTGCTGTCCGAAAGAGTGTGGCCATCGCCCGGGCCGAGGAAAGGCCG 463  
Db 160 GGGGTGTGCTGCTGTCCGAAAGAGTGTGGCCATCGCCCGGGCCGAGGAAAGGCCG 219  
Qy 464 GCGGTGTGAGAGCCGCTGAGTGTGTGAGCAATGAAACCACTCTACTCCCGCTGG 523  
Db 220 GCGGTGTGAGAGCCGCTGAGTGTGTGAGCAATGAAACCACTCTACTCCCGCTGG 279  
Qy 524 GAACTGTGATCCCGGAGTGTGTGAGCAATGAAACCACTCTACTCCCGCTGG 583  
Db 280 GAACTGTGATCCCGGAGTGTGTGAGCAATGAAACCACTCTACTCCCGCTGG 339  
Qy 584 GTGATGAGTCACTATCTTCCGAGCTGAGTGTGTGAGCAATGAAACCACTCTACTCC 643  
Db 340 GTGATGAGTCACTATCTTCCGAGCTGAGTGTGTGAGCAATGAAACCACTCTACTCC 399  
Qy 644 GATGAGCCCGGAGTGTGTGAGCAATGAAACCACTCTACTCCCGCTGG 703  
Db 400 GATGAGCCCGGAGTGTGTGAGCAATGAAACCACTCTACTCCCGCTGG 459  
Qy 704 GACAAAGAGAGCTTTTGGCACTGACTGCGCGGTGTCTGACACCTCCAGAACGAGATGC 763  
Db 460 GACAAAGAGAGCTTTTGGCACTGACTGCGCGGTGTCTGACACCTCCAGAACGAGATGC 519  
Qy 764 TGGGCGCCGTTCTGCTGGAGCCCGGGAGCTCTCTGCGGAGCCGAGCGAGGGA 823  
Db 520 TGGGCGCCGTTCTGCTGGAGCCCGGGAGCTCTCTGCGGAGCCGAGCGAGGGA 579  
Qy 824 TGGGCGCCGTTCTGCTGGAGCCCGGGAGCTCTCTGCGGAGCCGAGCGAGGGA 883  
Db 580 TGGGCGCCGTTCTGCTGGAGCCCGGGAGCTCTCTGCGGAGCCGAGCGAGGGA 639  
Qy 884 TGGGTCTCAG 943  
Db 640 TGGGTCTCAG 699  
Qy 944 CACCAAGTGGGCGAGCTGACCTGCTCCAGCCGAGCCGAGGTTCTAGGCTTTTACG 1003  
Db 700 CACCAAGTGGGCGAGCTGACCTGCTCCAGCCGAGCCGAGGTTCTAGGCTTTTACG 758  
Qy 1004 AGGCTGAG 1063  
Db 759 AGGCTGAG 818  
Qy 1064 GGTCTTCTGCTGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1122  
Db 819 GGTCTTCTGCTGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 878  
Qy 1123 GATATAGAGTTTGTATCTTTTATACAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1182  
Db 879 GATATAGAGTTTGTATCTTTTATACAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 937  
Qy 1183 ATTTAACTTTTATTTAAAGTT 1203  
Db 938 ATTTAACTTTTATTTAAAGTT 958

RESULT 2  
US-08-466-127-1  
Sequence 1, Application US/08466127  
Patent No. 5683878

## GENERAL INFORMATION:

APPLICANT: Elimeier, Willfried  
APPLICANT: Weith, Andreas  
TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kesseler, Goldstein & Fox P.L.L.C.  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington

STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,127  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Basmont, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 0652,1360002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 982 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 37..481  
US-08-466-127-1

Query Match 71.2%; Score 856.2; DB 1; Length 982;  
Best Local Similarity 97.7%; Pred. No. 5.7e-231;  
Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

Qy 284 GAGCGTGGCGGCGGTGAGAGTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 343  
Db 40 GATCTGACACAG 99  
Qy 344 GCACTCTGAGTCACTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 403  
Db 100 GCACTCTGAGTCACTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 159  
Qy 404 GCGGTGTGCTGCTGTCCGAAAGAGTGTGGCCATCGCCCGGGCCGAGGAAAGGCCG 463  
Db 160 GCGGTGTGCTGCTGTCCGAAAGAGTGTGGCCATCGCCCGGGCCGAGGAAAGGCCG 219  
Qy 464 GCGGTGTGCTGCTGTCCGAAAGAGTGTGGCCATCGCCCGGGCCGAGGAAAGGCCG 219  
Db 220 GCGGTGTGCTGCTGTCCGAAAGAGTGTGGCCATCGCCCGGGCCGAGGAAAGGCCG 279  
Qy 524 GAACTGTGATCCCGGAGTGTGTGAGCAATGAAACCACTCTACTCCCGCTGG 583  
Db 280 GAACTGTGATCCCGGAGTGTGTGAGCAATGAAACCACTCTACTCCCGCTGG 339  
Qy 584 GTGATGAGTCACTATCTTCCGAGCTGAGTGTGTGAGCAATGAAACCACTCTACTCC 643  
Db 340 GTGATGAGTCACTATCTTCCGAGCTGAGTGTGTGAGCAATGAAACCACTCTACTCC 399  
Qy 644 GATGAGCCCGGAGTGTGTGAGCAATGAAACCACTCTACTCCCGCTGG 703  
Db 400 GATGAGCCCGGAGTGTGTGAGCAATGAAACCACTCTACTCCCGCTGG 459  
Qy 704 GACAAAGAGAGCTTTTGGCACTGACTGCGCGGTGTCTGACACCTCCAGAACGAGATGC 763  
Db 460 GACAAAGAGAGCTTTTGGCACTGACTGCGCGGTGTCTGACACCTCCAGAACGAGATGC 519  
Qy 764 TGGGCGCCGTTCTGCTGGAGCCCGGGAGCTCTCTGCGGAGCCGAGCGAGGGA 823  
Db 520 TGGGCGCCGTTCTGCTGGAGCCCGGGAGCTCTCTGCGGAGCCGAGCGAGGGA 579  
Qy 824 TGGGCGCCGTTCTGCTGGAGCCCGGGAGCTCTCTGCGGAGCCGAGCGAGGGA 883

Db 580 TGGGCCCAACTCGCCCTGACCTTACCAAAATCCCTTCTGGAGACTGAACC 639  
Qy 884 TGGTCTCAGAGCGAAGAACTGTGAACCTTGTAGCTTGAAGCCAGAGACTAGCTTGGC 943  
Db 640 TGGTCTCAGAGCGAAGAACTGTGAACCTTGTAGCTTGAAGCCAGAGACTAGCTTGGC 699  
Qy 944 CACGAGCTGGGAGAGCTCAACCTGCTCCACCCCAAGTTCTAAGTCTTTTTCAG 1003  
Db 700 CACGAGCTGGGAGAGCTCAACCTGCTCCACCCCAAGTTCTAAGTCTTTTTCAG 758  
Qy 1004 ACCGTGAGAGTGTGAAGAGAGTGTGTCTCTCAACTATGCGCAAGCGCGAGAGCT 1063  
Db 759 ACCGTGAGAGTGTGAAGAGAGTGTGTCTCTCAACTATGCGCAAGCGCGAGAGCT 818  
Qy 1064 GGTCTTCTGCTCTCTTGTGAAGAAAGTTCTGTGGCCCTGATTTAAGTCTATATAG- 1122  
Db 819 GGTCTTCTGCTCTCTTGTGAAGAAAGTTCTGTGGCCCTGATTTAAGTCTATATAG 878  
Qy 1123 GATATAGAGTTTGTACCTTTTTCAGGGAGGTGACTTCTGTACAAATGCGATGTAT 1182  
Db 879 GATATAGAGTTTGTACCTTTTTCAGGGAGGTGACTTCTGTACAAATGCGATGTAT 937  
Qy 1183 ATTAACCTTTTATATAAGTT 1203  
Db 938 ATTAACCTTTTATATAAGTT 958

RESULT 3  
US-09-919-039-214  
; Sequence 214, Application US/09919039  
; Patent No. 6727066  
; GENERAL INFORMATION:  
; APPLICANT: Kaser, Matthew R.  
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES  
; FILE REFERENCE: PA-0035 US  
; CURRENT APPLICATION NUMBER: US/09/919,039  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: 60/222,113  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 401  
; SOFTWARE: PERL Program  
; SEQ ID NO 214  
; LENGTH: 653  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6727066 253987.16  
US-09-919-039-214

Query Match 36.4%; Score 437.8; DB 4; Length 653;  
Best Local Similarity 97.2%; Pred. No. 2.4e-113;  
Matches 456; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 736 TGTCTGACACCTCCAGAGCGAGGTGCTGGCCCGCTTCTGCTGGAGCCCGGGAGACC 795  
Db 147 TTTCTCTCCCGCCCGAGAGCGAGGTGCTGGCCCGCTTCTGCTGGAGCCCGGGAGACC 206  
Qy 796 TCTCTGCGGAGCGAGCGAGCGAGGTGCTGGCCCGCTTCTGCTGGAGCCCGGGAGACC 855  
Db 207 TCTCTGCGGAGCGAGCGAGCGAGGTGCTGGCCCGCTTCTGCTGGAGCCCGGGAGACC 266  
Qy 856 CACCAAAATCTCTCTGAGACTAACTGTGTCTCAGAGCGAAGAGACTGTGAACCTTGT 915  
Db 267 CACCAAAATCTCTCTGAGACTAACTGTGTCTCAGAGCGAAGAGACTGTGAACCTTGT 326  
Qy 916 ACCGTGAGAGCGAGCGAGGTGCTGGCCCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 975  
Db 327 GGCCTGAAAGCGAGCGAGGTGCTGGCCCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG 386  
Qy 976 CCAACCCCAAGTCTTAAGTCTTTTTCAGAGCGGTGAGAGTGTGAAGAGAGTGGCTCTTC 1035  
Db 387 CCAACCCCAAGTCTTAAGTCTTTTTCAGAGCGGTGAGAGTGTGAAGAGAGTGGCTCTTC 446

Qy 1036 CAACATAGCCAGGCGGCGAGAGCTGTCTTCTGCTCTTGGAGAAAGTTCTGT 1095  
Db 447 CAACATAGCCAGGCGGCGAGAGCTGTCTTCTGCTCTTGGAGAAAGTTCTGT 506  
Qy 1096 TGCCCTGATTTATGAACTCTATATAG-GTATATAGTTTGTACCTTTTTCAGGAA 1154  
Db 507 TGCCCTGATTTATGAACTCTATATAGAGTATATAGTTTGTACCTTTTTCAGGAA 566  
Qy 1155 GGTGACTTCTGTAACAATGCGATGTATTAACCTTTTATATAAGTT 1203  
Db 567 GGTGACTTCTGTAACAATGCGATGTATTAACCTTTTATATAAGTT 615

RESULT 4  
US-08-256-077-3  
; Sequence 3, Application US/08256077  
; Patent No. 5654188  
; GENERAL INFORMATION:  
; APPLICANT: Elmeyer, Wilfried  
; APPLICANT: Weith, Andreas  
; TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene  
; NUMBER OF SEQUENCES: 6  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/256,077  
; FILING DATE: 23-JUNE-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bemd, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 0652.1360000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 360 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-256-077-3

Query Match 29.9%; Score 360; DB 1; Length 360;  
Best Local Similarity 100.0%; Pred. No. 1.4e-91;  
Matches 360; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 368 ATGAAGGCGCGAGCGGCTGTGCGGCTGCTACAGAGCGGCTGTGCTGCTGCGAAGCC 427  
Db 1 ATGAAGGCGCGAGCGGCTGTGCGGCTGCTACAGAGCGGCTGTGCTGCTGCGAAGCC 60  
Qy 428 AGTCTGCGCATGCGCCCGGCGAGGAAAGGCGCGAGCTGAGAGAGCCGCTGAGCTTG 487  
Db 61 AGTCTGCGCATGCGCCCGGCGAGGAAAGGCGCGAGCTGAGAGAGCCGCTGAGCTTG 120  
Qy 488 CTGAGCAGCATGAACCATGCTACTCCCGCTGCGGGAAGTGTACCCGGAATCCCGAGA 547  
Db 121 CTGAGCAGCATGAACCATGCTACTCCCGCTGCGGGAAGTGTACCCGGAATCCCGAGA 180  
Qy 548 GGCACCTGAGCTTAGCGAGGTGAAGTCTTACAGCGCGTCACTGACTTCTGACCTG 607



Db 318 AGAGCGTGCCTTCCAGGAGGCTCTATAGTGAACCGCGCGG---GACAGTGGCCCGTG 374  
QY 300 CAGGTCACTGTAGC-GGACTTTCTTTGGTTTCTTTCTTTGGGGCACTCTGACTCA 358  
Db 375 CAGGTCACTGTAGCGGAGCTTTTGGTTTCTTTCTTTGGGGCACTCTGACTCA 434  
QY 359 CTCCCCAGCATG 370  
Db 435 CTCCCCAGCATG 446

## RESULT 7

US-08-466-127-5  
; Sequence 5, Application US/08466127  
; Patent No. 5683878  
; GENERAL INFORMATION:  
; APPLICANT: Eilmeier, Wilfried  
; APPLICANT: Melth, Andreas  
; TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,127  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bemond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 0652.1360002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 446 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; US-08-466-127-5

Query Match 25.5%; Score 306.4; DB 1; Length 446;  
Best Local Similarity 94.4%; Pred. No. 1.8e-76;  
Matches 351; Conservative 0; Mismatches 16; Indels 5; Gaps 3;  
QY 1 GATCTGGGCTGCTGCAGGAAAAAGCAATTCTGAAAGTTAATGTTTGAAGTATCTT 60  
Db 78 GATCTGGGCTGCTGCAGGAAAAAGCAATTCTGAAAGTTAATGTTTGAAGTATCTT 137  
QY 61 AAATCTTGTCTGGCGGAGAGCGCCGCTTCCCCGGATACAGCGCTTCTCATTTCTTGA 120  
Db 138 AAATCTTGTCTGGCGGAGAGAGCCCACTCTCCCCGGATACAGCACTTCTCATTTCTTGT 197  
QY 121 ATCCGGGCTCCGGGCTTTCGGCGTACAGCCAGCGGAGAAAGCTGTTTGCAATTTA 180  
Db 198 ATCCAGGCTCCGGGCTTTCGGCGTACAGCCAGCGGAGAAAGCTGTTTGCAATTTA 257  
QY 181 GCGGGCTGTGAACGCCAGGCGCGGCGGGGCGGGGCCGA-GCGGGCCATTGTAATTA 239  
Db 258 GCGGGCTGTGTACACCCAGGCGCGAGCGGGGCGGGGCCGAGGGCCATTGTAATTA 317

QY 240 AGAGCGTGCCTTCCAGGAGGCTCTATAGTGAACCGCGCGGAGCGTGGCCCGTGG 299  
Db 318 AGAGCGTGCCTTCCAGGAGGCTCTATAGTGAACCGCGCGG---GACAGTGGCCCGTG 374  
QY 300 CAGGTCACTGTAGC-GGACTTTCTTTGGTTTCTTTCTTTGGGGCACTCTGACTCA 358  
Db 375 CAGGTCACTGTAGCGGAGCTTTTGGTTTCTTTCTTTGGGGCACTCTGACTCA 434  
QY 359 CTCCCCAGCATG 370  
Db 435 CTCCCCAGCATG 446

## RESULT 8

US-09-513-999C-23008  
; Sequence 23008, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclet, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59, US2, REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent .pm  
; SEQ ID NO 23008  
; LENGTH: 255  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 42  
; OTHER INFORMATION: w=a or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 108  
; OTHER INFORMATION: w=a or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 220  
; OTHER INFORMATION: n=a, g, c or t  
; US-09-513-999C-23008

Query Match 16.5%; Score 198.4; DB 4; Length 255;  
Best Local Similarity 99.0%; Pred. No. 3.5e-46;  
Matches 199; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCTGGGCTGCTGCAGGAAAAAGCAATTCTGAAAGTTAATGTTTGAAGTATCTT 60  
Db 51 GATCTGGGCTGCTGCAGGAAAAAGCAATTCTGAAAGTTAATGTTTGAAGTATCTT 110  
QY 61 AAATCTTGTCTGGCGGAGAGCGCCGCTTCCCCGGATACAGCGCTTCTCATTTCTTGA 120  
Db 111 AAATCTTGTCTGGCGGAGAGAGCGCCGCTCTCCCCGGATACAGCGCTTCTCATTTCTTGA 170  
QY 121 ATCCGGGCTCCGGGCTTTCGGCGTACAGCCAGCGGAGAAAGCTGTTTGCAATTTA 180  
Db 171 ATCCGGGCTCCGGGCTTTCGGCGTACAGCCAGCGGAGAAAGCTGTTTGCAATTTA 230  
QY 181 GCGGGCTGTGAACGCCAGG 201  
Db 231 GCGGGCTGTGAACGCCAGG 251

RESULT 9  
US-08-151-391A-3  
; Sequence 3, Application US/08151391A  
; Patent No. 5527897

```

; GENERAL INFORMATION:
; APPLICANT: Oda, Kinichiro
; APPLICANT: Nakada, Susumu
; APPLICANT: Hara, Eiji
; APPLICANT: Yamaguchi, Tomoko
; APPLICANT: Nakamura, Takeshi
; APPLICANT: Oka, Yumiko
; APPLICANT: Kishimoto, Toshiko
; TITLE OF INVENTION: Human ID Genes
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,391A
; FILING DATE: 12-NOV-1993
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Mills, Demetria J.
; REGISTRATION NUMBER: 34,506
; REFERENCE/DOCKET NUMBER: 715-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)684-1111
; TELEFAX: (703)684-1124
; TELEX: 82-4425
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 22..465
; OTHER INFORMATION: /note="CDS"
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US-08-151-391A-3

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Best Local Similarity 58.0%; Pred. No. 2,4e-11;
Matches 163; Conservative 0; Mismatches 100; Indels 18; Gaps 1;

QY      369 TGAAGCGCTGAGCCCGGCTGCGCTCTACGAGCGCGTGTGCTGCTGCTGCGAAGCCA 428
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DB      77 TGAAGCGCGGGAAGACAGAGCGGCTGGGGGAGAGTGTGCTGTCTGTGAGCAGA 136
      |||||
QY      429 GTCTGGCCATGCGCCCGGGCCGAGGGAAGGGCCCGGCACGTGAGGAGCCGCTGAGCT--- 485
      |||||
DB      137 GCGTGGCCATCTCGCGCTGCCCGGGCGCGCGCTGCTGCTGCTGCGAGCAGC 196
      |||||
QY      486 -----TGTGAGCAGCATGAACCACTGCTACCTCCGCGCTGGGGGAAGCTGG 530
      |||||
DB      197 AGCAGGTAACGTGCTGCTCTACGACATGAACGGCTGTACTACGCTCAAGAGAGCTGG 256
      |||||
QY      531 TACCGGAGTCCCGAGAGCACTCAGCTTAGCGCAGGTGAAATCTTACAGGCGCTGATCG 590
      |||||
DB      257 TGCCCAACCTGCGCCAGAACCGCAAGGTGAGCAAGTTCTTCCAGCAGCTGATCG 316
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QY      591 ACTACATTCTGACCTGAGGAGTGTCTTGGCCGAGCCAGCC 631
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DB      317 ACTACATGAGGAGCCTTCAAGTTGAGCTGAATTC 357
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RESULT 10
US-09-561-497-3
; Sequence 3, Application US/09561497
; Patent No. 6372433
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: C. Frank Bennett
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR OF DNA BINDING-1 EXPRESSION
; FILE REFERENCE: RTS-0149
; CURRENT APPLICATION NUMBER: US/09/561,497
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (36)...(500)
;
US-09-561-497-3

Query Match      6.2%; Score 75; DB 3; Length 926;
Best Local Similarity 58.0%; Pred. No. 3,1e-11;
Matches 163; Conservative 0; Mismatches 100; Indels 18; Gaps 1;

QY      369 TGAAGCGCTGAGCCCGGCTGCGCTCTACGAGCGCGTGTGCTGCTGCTGCGAAGCCA 428
      |||||
DB      91 TGAAGCGCGGGAAGACAGAGCGGCTGGGGGAGAGTGTGCTGTCTGTGAGCAGA 150
      |||||
QY      429 GTCTGGCCATGCGCCCGGGCGCGAGGGAAGGGCCCGGCAGCTGAGGAGCCGCTGAGCT--- 485
      |||||
DB      151 GCGTGGCCATCTCGCGCTGCCCGGGCGCGCGCTGCTGCTGCTGCTGAGCAGC 210
      |||||
QY      486 -----TCTGAGCAGCATGAACCACTGCTACCTCCGCGCTGGCGGAAGCTGG 530
      |||||
DB      211 AGCAGGTAACGTGCTGCTCTCTACGACATGAACGGCTGTACTACGCTCAAGAGAGCTGG 270
      |||||
QY      531 TACCGGAGTCCCGAGAGCACTCAGCTTAGCCAGGTGAAATCTTACAGGCGCTGATCG 590
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DB      271 TGCCCAACCTGCGCCAGAACCGCAAGGTGAGCAAGTTCTTCCAGCAGCTGATCG 330
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QY      591 ACTACATTCTGACCTGAGGAGTGTCTTGGCCGAGCCAGCC 631
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DB      331 ACTACATGAGGAGCCTTCAAGTTGAGCTGAATTC 371
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RESULT 11
US-08-151-391A-1
; Sequence 1, Application US/08151391A
; Patent No. 5527897
; GENERAL INFORMATION:
; APPLICANT: Oda, Kinichiro
; APPLICANT: Nakada, Susumu
; APPLICANT: Hara, Eiji
; APPLICANT: Yamaguchi, Tomoko
; APPLICANT: Nakamura, Takeshi
; APPLICANT: Oka, Yumiko
; APPLICANT: Kishimoto, Toshiko
; TITLE OF INVENTION: Human ID Genes
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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1  SOFTWARE: PatentIn Release #1.0, Version #1.25
2  CURRENT APPLICATION DATA:
3  APPLICATION NUMBER: US/08/151,391A
4  FILING DATE: 12-NOV-1993
5  CLASSIFICATION: 536
6  ATTORNEY/AGENT INFORMATION:
7  NAME: Mills, Demetra J.
8  REGISTRATION NUMBER: 34,506
9  REFERENCE/DOCKET NUMBER: 715-087
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (703)684-1111
12 TELEFAX: (703)684-1124
13 TELEX: 82-4425
14 INFORMATION FOR SEQ ID NO: 1:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 509 base pairs
17 TYPE: nucleic acid
18 STRANDEDNESS: double
19 TOPOLOGY: linear
20 MOLECULE TYPE: cDNA to mRNA
21 HYPOTHEetical: NO
22 ANTI-SENSE: NO
23 ORIGINAL SOURCE:
24 ORGANISM: Homo sapiens
25 FEATURE:
26 NAME/KEY: misc feature
27 LOCATION: 22..483
28 OTHER INFORMATION: /note="CDS"
29
30 US-08-151-391A-1

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Query Match 6.1%; Score 73.4; DB 1; Length 509;

QY	369	TGAAGGCGGTGAGCCCGGTGGCGGCGCTGTACTACGAGCGGTGTGCTCTCGTTCGGAACGCA	428
Db	77	TGAAGGCGGGAAGACAGCGAGCGGTGGCGGCGGAGGTGGTGGCGCTGTCTGTCTGAGAGAA	136
QY	429	GTCCTGGCCATTCGCGCCGGGGCCCGAAGGAAGGCCCGGCAGCTGAGAGACCGCTAGCT---	485
Db	137	GCGTGGCCATCTCGCGCTGCCCGGGGGCGCGCGCTGGCTGCTGTGGAAGAGC	196
QY	486	-----TGCTGGAAGCATGAAACCACTGCTACTCCGCGCTGGGGAACCTGG	530
Db	197	AGCAGGTAAACGTGCTGCTCTTACGACATGAACGGCTGTTACTACGCGCTTAAGAAAGCTGG	256
QY	531	TACCGGAGTCCCGAAGGCACTCAGCTTAGCCAGGTGGAATCTCAACGCGGCTATCG	590
Db	257	TGCCCAACCTGCCCCGAAACCGCAAGGTGAGCAAGGTGAGATTTCTCCAGCAGTCATCG	316
QY	591	ACTACATCTCGACCTGCAAGTAGTACTCTGGCCGACGCAAGC	631
Db	317	ACTACATCAGGACCTTCAGTTGACGCTGAATCTCGGAATCC	357

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RESULT 12
US-09-561-497-10
; Sequence 10, Application US/09561497
; Patent No. 637243
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: C. Frank Bennett
; TITLE OF INVENTION: ANTISENSE MODULATION OF DNA BINDING-1 EXPRESSION
; FILE REFERENCE: RTS-0149
; CURRENT APPLICATION NUMBER: US/09/561,497
; CURRENT FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 10
; LENGTH: 4793
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

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; NAME/KEY: CDS
; LOCATION: (2210)... (2659)
US-09-561-497-10

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Query Match	5.8%;	Score 70;	DB 3;	Length 4793;
Best Local Similarity	59.2%;	Pred. No. 1.6e-09;		
Matches 168;	Conservative 0;	Mismatches 95;	Indels 21;	Gaps 21;

Oy	369	TGAAGCGCCTAGCCGGGTGCGCGACTCTACGAGGCAGTGTGCTGTGGAAACGA	428
Db	2265	TGAAGCCCGGCAAGACACAGCAGCCGTGGGGCGAAGTGATGTCGTGTAGACAGA	232
Oy	429	GTCGTGCCATCGCCCGGGGCCGAGGGAAGGCCCGCGCA-----GCTG	470
Db	2335	GCGTGGCATTTCCGCTGCGCCCGGGGGCGCCGGGGCCGCGCTGCTGCCCTGTGGACG	2384
Oy	471	AGGAGCGCGCTAGGTTGCTG---GACGACATGAACAATGTGCATCTCCGCGTCGGGAAAC	527
Db	2385	AGCAGCAGGTAAAGTGTCTCTACACACATGMAAGGCTGTATTCTCAGCGCTCAAAGAAC	244
Oy	528	TGGTACC CGAGTCCC GAGAGCACTCAGCTTAAGCAGGTGAAA TCTTA CAGCGCTCA	587
Db	2445	TGGTGCCCA CCTCTCC CAGAA CGCAGAGGTAGACAA GTGAGATTTCTCCAGCACGTCA	2504
Oy	588	TCGACTACATCTGACCTCGAGGTAAGCTCGGCGGACCAAGCC	631
Db	2505	TCGACTACATCAGGACCTTACGATTGGAGCTGAATCGGAATCC	2548

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RESULT 13
US-08-896-164-30
; Sequence 30, Application US/08896164
; Patent No. 6218521
; GENERAL INFORMATION:
; APPLICANT: OBATA, Yuichi
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES ASSOCIATED
; TITLE OF INVENTION: WITH GASTRIC CANCER AND METHODS FOR
; TITLE OF INVENTION: DIAGNOSING AND TREATING GASTRIC CANCER
; NUMBER OF SEQUENCES: 87
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Falfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44mb
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,164
; FILING DATE: July 17, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6218521man D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5499 - JEL/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 721 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; US-08-896-164-30
;
; Query Match 5.7%; Score 69; DB 3; Length 721;
; Best Local Similarity 58.8%; Pred. No. 1.4e-09;
; Matches 167; Conservative 0; Mismatches 96; Indels 21; Gaps 2

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QY 369 TGAAGCGCTGAGCCCCGCGCGCTGCTACGACCGGTGTGCTGCTGCTGCGAAGCA 428  
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DB 118 TGAAGCGCGGCAAGACAGGACGGTTCGGCGCGAAGGTGTGCTGCTGAGCA 177  
| | | | |  
QY 429 GTCTGCGCATCCGCGCGGCGCGAAGGCGCCGCA-----GCTG 470  
| | | | |  
DB 178 GGTGGCCATCTCGCGCTCGCGCGGGGGCGCGCGCTGCTGCTGCGACG 237  
| | | | |  
QY 471 AGGAGCCGCTGAGCTTGTCTG---GACGACATGACCACTGCTCTCCGCTGCGGAAC 527  
| | | | |  
DB 238 AGCAGCAGGTAAACGTGCTGCTCTACNACATGAAAGCGCTGTACTCAGCGCTCAAGAGAC 297  
| | | | |  
QY 528 TGGTACCGGAGTCCCGAGAGGCACTCAAGCTAGCGAGGTGGAATCTTACAGCGCGTCA 587  
| | | | |  
DB 298 TGGTCCCACTCGCGCCCAAGAACCCGAAAGGTGAGCAAGGTGGAATCTTCCAGCAGTCA 357  
| | | | |  
QY 588 TCGACTACATTTCTGACCTGCAAGTGTAGTCTGCGCGAGCCAGCC 631  
| | | | |  
DB 358 TCGACTACATCAAGGACCTTGTGTTGAGGCTGAATCGGAATCC 401  
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## RESULT 14

US-09-621-976-2005  
; Sequence 2005, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 2005  
; LENGTH: 626  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 211..570  
; NAME/KEY: s1g\_peptide  
; LOCATION: 211..378  
; OTHER INFORMATION: von Heijne matrix  
; OTHER INFORMATION: score 3.5999990463257  
; OTHER INFORMATION: seq IQ1ALGLAFLX/DL  
US-09-621-976-2005

Query Match 5.2%; Score 62.8; DB 4; Length 626;

Best Local Similarity 55.1%; Pred. No. 7.1e-08;  
Matches 173; Conservative 7; Mismatches 125; Indels 9; Gaps 3;

QY 412 CTGCTGTGGAACCGAGTCTGCGCATCGCCCGGCGCGAAGGAGCGCGGAGCTGA 471  
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DB 152 CAGCTGTGCGACCAACAGCTGGGATCTTAMCGAAGAAACCCCTGTGACGACCCGA 211  
| | | | |  
QY 472 GAGCGCGTGAAGCTTGTGAGACATGAACCACTGTACTCCGCTCGCGGAACTGT 531  
| | | | |  
DB 212 TGAGG-----CTGKSTATACATGATGACGACTGTACTCAAGCTCAAGAGAGCTGT 264  
| | | | |  
QY 532 ACCCGAGTCCCGAAGGCACTCAGTTAGCCAGGTGGAATCTTCAAGCGCGT-CATCG 590  
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DB 265 GCCCGAGATCCCGCAAGACAGAGGTAGCAAGATGAAATCTTCCGACGATCATWG 324  
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QY 591 ACTACAT-TCTGACCTGAGGTAGTCTTGGCGGAGCCGCTGAGACCCCTGATGAC 649  
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DB 325 ACTACATCTTGGGACCTGAGATGCGCTGGGACTCGATGCCACTTTGTGSAAGACTG 384  
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QY 650 CCCGACTTTCCCATCAAGACAGCGAGCTCGCTCCGGAACCTTGTGATTTCCAGCAGCAA 709  
| | | | |  
DB 385 CATCACCAAGAACCCGGGGGAGAAACAGAGGCTTCAGAGCGCGGCTTGAACCACTCTAAC 444  
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QY 710 AGAGCTTTTGCCA 723  
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DB 445 ACGGATATACGCA 458  
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## RESULT 15

US-08-362-495-4  
; Sequence 4, Application US/08362495  
; Patent No. 6087171  
; GENERAL INFORMATION:  
; APPLICANT: Neuman, Toomas  
; APPLICANT: Suda, Kikuo  
; APPLICANT: No. 6087171nes, Howard O.  
; TITLE OF INVENTION: METHOD FOR INDUCING DNA SYNTHESIS IN  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESS: Dunnet, L.L.P.  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/362,495  
; FILING DATE: 18-NOV-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US94/14614  
; FILING DATE: 19-DEC-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/301,416  
; FILING DATE: 08-SEP-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/169,522  
; FILING DATE: 15-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Barker, M. Paul  
; REGISTRATION NUMBER: 32,013  
; REFERENCE/DOCKET NUMBER: 05800.0001-02000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1309 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-362-495-4

Query Match 4.0%; Score 47.6; DB 3; Length 1309;

Best Local Similarity 57.0%; Pred. No. 0.0018;  
Matches 106; Conservative 0; Mismatches 79; Indels 1; Gaps 1;

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DB 388 AGGCGCGCGAGTGAACCCGCGCTGTGCTGACGTGCAATGAAACGACTGCTACAGTC 447  
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QY 516 GCGTGGAGGAACGTGTCGCCGAGTCCCGAAGGCACTGAGCTTACGAGGTGGAATCC 575  
| | | | |  
DB 448 G-CTGCGAAGGCTGTCTTACCAATCCGCGCAACAGAAAGTCAAGCAAGTGAATCC 506  
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QY 576 TACAGCGCTGATGACTGATTAATTCGACCTGCAAGGTAGTCTTGGCCGACGCGCCCTG 635  
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Qy	636	GACCCC	641
Db	567	CTCTCC	572

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
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Title: US-09-996-529A-5

Perfect score: 1203

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Searched: 4093002 seqs, 276041825 residues

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Minimum DB seq length: 0

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Maximum Match 100%  
Listing first 45 summaries

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- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
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- 20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1178.4	98.0	1203	US-10-171-581-258	Sequence 258, App
2	1178.4	98.0	1203	US-10-450-826-22	Sequence 22, App1
3	1164.2	96.8	2066	US-10-116-802-341	Sequence 341, App
4	1164.2	96.8	2066	US-10-084-817-263	Sequence 263, App
5	1162.8	96.7	1300	US-09-925-298-39	Sequence 39, App1
6	1162.8	96.7	1300	US-10-103-806-39	Sequence 39, App1
7	950.8	79.0	1504	US-10-198-846-13483	Sequence 13483, A
8	856.2	71.2	982	US-10-450-826-21	Sequence 21, App1
9	652.8	54.3	2481	US-10-450-826-23	Sequence 23, App1
10	437.8	36.4	653	US-09-919-039-214	Sequence 214, App
11	437.8	36.4	653	US-10-116-802-341	Sequence 341, App
12	437.8	36.4	2066	US-10-116-802-341	Sequence 341, App

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	15	422.6	35.1	429	10	US-09-918-995-8760	Sequence 8760, App
	16	358.4	29.8	360	17	US-10-384-339C-88	Sequence 88, App1
	17	354	29.4	531	15	US-10-029-386-9621	Sequence 9621, App
	18	345.8	28.7	568	16	US-10-152-319A-1595	Sequence 1595, App
	19	335.4	27.9	517	18	US-10-363-345A-26392	Sequence 26392, A
	20	335.4	27.9	517	18	US-10-363-345A-26392	Sequence 26392, A
	21	309	25.7	495	9	US-09-864-761-19607	Sequence 19607, A
	22	296.2	24.6	517	18	US-10-363-345A-26390	Sequence 26390, A
	23	296.2	24.6	517	18	US-10-363-345A-26390	Sequence 26390, A
	24	285	23.7	285	15	US-10-029-386-9621	Sequence 9621, A
	25	258	21.4	258	9	US-09-796-692-9456	Sequence 9456, App
	26	258	21.4	258	14	US-10-040-662-9456	Sequence 9456, App
	27	258	21.4	258	16	US-10-057-475B-9456	Sequence 9456, App
	28	258	21.4	258	16	US-10-154-884B-9456	Sequence 9456, App
	29	258	21.4	258	17	US-10-764-324-9456	Sequence 9456, App
	30	246	20.4	528	16	US-10-388-934-658	Sequence 658, App
	31	189.6	15.8	247	16	US-10-242-535A-28198	Sequence 28198, A
	32	189.6	15.8	247	16	US-10-085-783A-28198	Sequence 28198, A
	33	171.6	14.3	926	14	US-10-198-846-871	Sequence 871, App
	34	144.4	12.0	215	16	US-10-242-535A-8033	Sequence 8033, App
	35	144.4	12.0	215	16	US-10-085-783A-8033	Sequence 8033, App
	36	125.8	10.5	337	17	US-10-469-285-573	Sequence 573, App
	37	121	10.1	133	9	US-09-815-343-13	Sequence 13, App1
	38	121	10.1	133	9	US-09-815-343-619	Sequence 619, App
	39	121	10.1	133	9	US-09-815-343-1374	Sequence 1374, App
	40	121	10.1	133	9	US-09-815-343-1432	Sequence 1432, App
	41	121	10.1	133	16	US-10-097-105-13	Sequence 13, App1
	42	121	10.1	133	16	US-10-097-105-619	Sequence 619, App1
	43	121	10.1	133	16	US-10-097-105-1374	Sequence 1374, App
	44	121	10.1	133	16	US-10-097-105-1432	Sequence 1432, App
	45	119.4	9.9	133	9	US-09-815-343-1000	Sequence 1000, App

ALIGNMENTS

RESULT 1  
US-10-171-581-258  
; Sequence 258, Application US/10171581  
; Publication No. US20030104426A1  
; GENERAL INFORMATION:  
; APPLICANT: Dai, Hongyue  
; APPLICANT: Linley, Peter  
; TITLE OF INVENTION: Signature Genes in Chronic Myelogenous Leukemia  
; FILE REFERENCE: 9301-157-999  
; CURRENT APPLICATION NUMBER: US/10/171,581  
; CURRENT FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: 60/298,914  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 366  
; SEQ ID NO 258  
; LENGTH: 1203  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: X69111  
; DATABASE ENTRY DATE: 2001-06-18  
US-10-171-581-258

Qy	1	GATCGGGGCTGCGCAGAAAGCAATTCGAAATTAAGTTTGAAGTATCTT	60
Qy	1	GATCGGGGCTGCGCAGAAAGCAATTCGAAATTAAGTTTGAAGTATCTT	60
Qy	1	AAATCTTCTGCGCGAGAGAGCCCGCTTCCTCCGATCAGCGCTTCCTATCTTGA	120
Qy	1	AAATCTTCTGCGCGAGAGAGCCCGCTTCCTCCGATCAGCGCTTCCTATCTTGA	120
Qy	1	AAATCTTCTGCGCGAGAGAGCCCGCTTCCTCCGATCAGCGCTTCCTATCTTGA	120

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QY 121 ATCCGAGGCTCCGCGGTCTTGGCGCTCAGACCAAGCCGAGAGAGCTGTGCAATTTAA 180
DB 121 ATCCGAGGCTCCGCGGTCTTGGCGCTCAGACCAAGCCGAGAGAGCTGTGCAATTTAA 180
QY 181 GCGGCGCTGTGAACGCCCAAGGCGCGGCGCGGCGCGAGAGCGGCGCATTTGAATTTAA 240
DB 181 GCGGCGCTGTGAACGCCCAAGGCGCGGCGCGGCGCGAGAGCGGCGCATTTGAATTTAA 240
QY 241 GAGGCGTCCCTCCAGGAGAGCTCTATATAGTACCCGCGCGCGAGCGGTGCGCGCTTGC 300
DB 241 GAGGCGTCCCTCCAGGAGAGCTCTATATAGTACCCGCGCGCGAGCGGTGCGCGCTTGC 300
QY 301 AGGTCACTGTAGCGGACTTTTGTGTTTCTTTCTCTTTGGGCGCACTCTGACTACT 360
DB 301 AGGTCACTGTAGCGGACTTTTGTGTTTCTTTCTCTTTGGGCGCACTCTGACTACT 360
QY 361 CCCAGCATGAAAGCGCTGAGCCGCGGTGCGCGCTGCTACGAGCGGTGCTGCTGCTGC 420
DB 361 CCCAGCATGAAAGCGCTGAGCCGCGGTGCGCGCTGCTACGAGCGGTGCTGCTGCTGC 420
QY 421 GGAACGAGTGTGCGCATCGCCGCGGCGCGAGGGAAGGCGCGCGCACTGAGAGCGCT 480
DB 421 GGAACGAGTGTGCGCATCGCCGCGGCGCGAGGGAAGGCGCGCGCACTGAGAGCGCT 480
QY 481 GAGCTTGTGAGCAGCATGAAACACTGCTA CTCGCGCTGCGGGAAGTGGTACCGGAGT 540
DB 481 GAGCTTGTGAGCAGCATGAAACACTGCTA CTCGCGCTGCGGGAAGTGGTACCGGAGT 540
QY 541 CCCGAGAGGAGCTAGCTTACGAGGAGGAAATCTTACAGCGCGTCTATGACTACTTCT 600
DB 541 CCCGAGAGGAGCTAGCTTACGAGGAGGAAATCTTACAGCGCGTCTATGACTACTTCT 600
QY 601 CGACTGTGAGTGTGCTGAGCCGAGCCAGCCCTGAGACCCCGGATGAGCCCGCACTTCC 660
DB 601 CGACTGTGAGTGTGCTGAGCCGAGCCAGCCCTGAGACCCCGGATGAGCCCGCACTTCC 660
QY 661 CATCCGAGAGCGGAGCTGCTCGGAACTTGTCTATCTTCAACGACAAAGAGCTTTTG 720
DB 661 CATCCGAGAGCGGAGCTGCTCGGAACTTGTCTATCTTCAACGACAAAGAGCTTTTG 720
QY 721 CCACTGACTGCGCGGTGCTGCACTCTCAGAGCAGAGTGTGCGCGCTTGTGCT 780
DB 721 CCACTGACTGCGCGGTGCTGCACTCTCAGAGCAGAGTGTGCGCGCTTGTGCT 780
QY 781 GGGAGCCCGGGAACCTTCTCTGCGGAGACCGGAGCGGAGTGGGCCCACTTGC 840
DB 781 GGGAGCCCGGGAACCTTCTCTGCGGAGACCGGAGCGGAGTGGGCCCACTTGC 840
QY 841 CTGCGCACTTGACTTACCAAAATCCCTTCTGAGAGACTTAACTTGTGCTCAGAGCGAA 900
DB 841 CTGCGCACTTGACTTACCAAAATCCCTTCTGAGAGACTTAACTTGTGCTCAGAGCGAA 900
QY 901 GGAAGTGTGAATTTGAGCTGAGAGCAGAGCTAGCTCTGCGCAACGAGTGGCGACGT 960
DB 901 GGAAGTGTGAATTTGAGCTGAGAGCAGAGCTAGCTCTGCGCAACGAGTGGCGACGT 960
QY 961 CACCGTGCACCAACCCCAAGCTTCTTCAAGTCTTTTCAAGAGCTGAGAGTGTGAA 1020
DB 961 CACCGTGCACCAACCCCAAGCTTCTTCAAGTCTTTTCAAGAGCTGAGAGTGTGAA 1020
QY 1021 GAGAGTGTGCTCTCAAACTATGCAAGGCGCGGCGAGCTGCTTCTGCGTCTCT 1080
DB 1021 GAGAGTGTGCTCTCAAACTATGCAAGGCGCGGCGAGCTGCTTCTGCGTCTCT 1080
QY 1081 GGAAGAAGTGTCTGTGCGCTGATTTATGAATCTTATATAG-STATATAGTGTGTAC 1139
DB 1081 GGAAGAAGTGTCTGTGCGCTGATTTATGAATCTTATATAGTGTGTGTGTGTAC 1139
QY 1140 CTTTTTTCAGGGAAGTGAATTTCTGTGAACAATGCAATGATATTTAACTTTTATATA 1199
DB 1140 CTTTTTTCAGGGAAGTGAATTTCTGTGAACAATGCAATGATATTTAACTTTTATATA 1199
QY 1141 CTTTTTTCAGGGAAGTGAATTTCTGTGAACAATGCAATGATATTTAACTTTTATATA 1199
DB 1141 CTTTTTTCAGGGAAGTGAATTTCTGTGAACAATGCAATGATATTTAACTTTTATATA 1199
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QY 1200 AGTT 1203
DB 1200 AGTT 1203

RESULT 2
US-10-450-826-22
; Sequence 22, Application US/10450826
; Publication No. US20040101818A1
; GENERAL INFORMATION:
; APPLICANT: JI, Darren
; APPLICANT: Axelrod, Douglas W.
; APPLICANT: Cook, Jonathan S.
; APPLICANT: Jalelwal, Neelam
; APPLICANT: Eistein, Richard
; APPLICANT: Houghton, Adam
; APPLICANT: Mertz, Lawrence
; TITLE OF INVENTION: Gene Expression Profiles Associated with Osteoblast Differentiation
; FILE REFERENCE: 044921-5039-WO
; CURRENT APPLICATION NUMBER: US/10/450,826
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/255,882
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/285,691
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. X69111
US-10-450-826-22

Query Match 98.0%; Score 1178.4; DB 17; Length 1203;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1201; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY 1 GATCTGGGGTGTGCTCCAGGAAAAAGCAATTTGGAAGTAAATGTTTGAATTTCT 60
DB 1 GATCTGGGGTGTGCTCCAGGAAAAAGCAATTTGGAAGTAAATGTTTGAATTTCT 60
QY 61 AAATCTTGTGCGCGGAGAGCGCCGCTTCTCCCGATACAGCGCTTCTCAATTTTGA 120
DB 61 AAATCTTGTGCGCGGAGAGCGCCGCTTCTCCCGATACAGCGCTTCTCAATTTTGA 120
QY 121 ATCCGCGGCTCCGCGGTCTTCCGCGTCAAGCAGCGGAGAGGCTGTTTGAATTTAA 180
DB 121 ATCCGCGGCTCCGCGGTCTTCCGCGTCAAGCAGCGGAGAGGCTGTTTGAATTTAA 180
QY 181 GCGGCGTGTGAACGCCCAAGGCGCGGCGCGGCGGAGCGGCGCATTTGAATTTAA 240
DB 181 GCGGCGTGTGAACGCCCAAGGCGCGGCGCGGCGGAGCGGCGCATTTGAATTTAA 240
QY 241 GAGGCGTGTGGAACGCCCAAGGCGCGGCGCGGCGGAGCGGCGCATTTGAATTTAA 240
DB 241 GAGGCGTGTGGAACGCCCAAGGCGCGGCGCGGCGGAGCGGCGCATTTGAATTTAA 240
QY 301 AGGTCACTGTAGCGGACTTTTGTGTTTCTTTCTCTTTGGGCGCACTCTGACTACT 360
DB 301 AGGTCACTGTAGCGGACTTTTGTGTTTCTTTCTCTTTGGGCGCACTCTGACTACT 360
QY 361 CCCAGCATGAAAGCGCTGAGCCGCGGTGCGCGCTGCTACGAGCGGTGCTGCTGCTGC 420
DB 361 CCCAGCATGAAAGCGCTGAGCCGCGGTGCGCGCTGCTACGAGCGGTGCTGCTGCTGC 420
QY 421 GGAACGAGTGTGCGCATCGCCGCGGCGCGAGGGAAGGCGCGCGCACTGAGAGCGCT 480
DB 421 GGAACGAGTGTGCGCATCGCCGCGGCGCGAGGGAAGGCGCGCGCACTGAGAGCGCT 480
QY 481 GAGCTTGTGAGCAGCATGAAACACTGCTA CTCGCGCTGCGGGAAGTGGTACCGGAGT 540
DB 481 GAGCTTGTGAGCAGCATGAAACACTGCTA CTCGCGCTGCGGGAAGTGGTACCGGAGT 540
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Db 481 GAGCTTGCTGACGACATGAAACCACTGCTACTCCGCGCTGCGGAACTGTACCCGGAGT 540
Qy 541 CCCGAGAGCACTAGCTTAAAGCCAGGTGAAATCTCTACAGCCGCTCATTCGATTAATCT 600
Db 541 CCCGAGAGCACTAGCTTAAAGCCAGGTGAAATCTCTACAGCCGCTCATTCGATTAATCT 600
Qy 601 CGAAGTGAAGTATGCTTGGAGCGAGCCGCTGGAACCCCTGATGAGCCGCCACTTCC 660
Db 601 CGAAGTGAAGTATGCTTGGAGCGAGCCGCTGGAACCCCTGATGAGCCGCCACTTCC 660
Qy 661 CATCCAGACAGCCGAGCTGCTCCGAACTTGTCTCAACGACAAAGAGAGCTTTTG 720
Db 661 CATCCAGACAGCCGAGCTGCTCCGAACTTGTCTCAACGACAAAGAGAGCTTTTG 720
Qy 721 CCACTGACTCGGCGCTGTCTTGAACACTTCAGAAAGCAGAGTGTGCGCCCTTCTGCT 780
Db 721 CCACTGACTCGGCGCTGTCTTGAACACTTCAGAAAGCAGAGTGTGCGCCCTTCTGCT 780
Qy 781 GGGAGCCCGGGAACCTCTGCGGAGCGGAGCGGAGGAGTGGGCCCCCACTTCGCC 840
Db 781 GGGAGCCCGGGAACCTCTCTGCGGAGCGGAGCGGAGGAGTGGGCCCCCACTTCGCC 840
Qy 841 CTGCCCACTTGAATTCAACCAATCCCTTCTGGAAGCTAAACCTGCTCTCAGAGCGAA 900
Db 841 CTGCCCACTTGAATTCAACCAATCCCTTCTGGAAGCTAAACCTGCTCTCAGAGCGAA 900
Qy 901 GGAAGTGAAGTGTGAGCTTGAAGAGCCAGAGCTGAGCTTGGCCACAGCTGGGCGAGCT 960
Db 901 GGAAGTGAAGTGTGAGCTTGAAGAGCCAGAGCTGAGCTTGGCCACAGCTGGGCGAGCT 960
Qy 961 CACCGTGCCTCCAGCCCAACCCCAAGTTCTAAGGCTTTTCAAGAGGTGGAAGTGGAA 1020
Db 961 CACCGTGCCTCCAGCCCAACCCCAAGTTCTAAGGCTTTTCAAGAGGTGGAAGTGGAA 1020
Qy 1021 GGAAGTGCCTCTCTCAAACTATGCGCAAGCGCGAGAGCTGTCTTCTGCTCTCT 1080
Db 1021 GGAAGTGCCTCTCTCAAACTATGCGCAAGCGCGAGAGCTGTCTTCTGCTCTCT 1080
Qy 1081 GGAGAAAGTTCCTGTTGCCCTGATTTATGAACTCTATATAG-CTATATAGTTTGTAC 1139
Db 1081 GGAGAAAGTTCCTGTTGCCCTGATTTATGAACTCTATATAG-CTATATAGTTTGTAC 1139
Qy 1140 CTTTTTACAGGAAAGTGAAGTTCCTGTAACAATGAGTAATTAACCTTTTATTA 1199
Db 1140 CTTTTTACAGGAAAGTGAAGTTCCTGTAACAATGAGTAATTAACCTTTTATTA 1199
Qy 1141 CTTTTTAA-AGAGTGAATTTCTGTAACAATGAGTAATTAACCTTTTATTA 1199
Db 1141 CTTTTTAA-AGAGTGAATTTCTGTAACAATGAGTAATTAACCTTTTATTA 1199
Qy 1200 AGTT 1203
Db 1200 AGTT 1203
Qy 1200 AGTT 1203
Db 1200 AGTT 1203
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RESULT 3
US-10-116-802-341
; Sequence 341, Application US/10116802
; Publication No. US20030065157A1
; GENERAL INFORMATION:
; APPLICANT: Amy Labek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
; CURRENT APPLICATION NUMBER: US/10/116,802
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 341
; LENGTH: 2066
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 253987.19
; NAME/KEY: unsure
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; LOCATION: 78, 112, 132, 148, 150, 157, 1405
; OTHER INFORMATION: a, t, c, g, or other
US-10-116-802-341
Query Match 96.8%; Score 1164.2; DB 14; Length 2066;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1199; Conservative 0; Mismatches 3; Indels 3; Gaps 3;
Qy 1 GATCTGGGCTCTGCGAGGAAAGCAATTCGTGAAGTAAATGTTTGTGATTCCT 60
Db 176 GATCTGGGCTCTGCGAGGAAAGCAATTCGTGAAGTAAATGTTTGTGATTCCT 235
Qy 61 AATCTCTGAGCGGAGAGGCGGCTCTCCCGGTATCAGCGCTTCCTCATTTTGA 120
Db 236 AATCTCTGAGCGGAGAGGCGGCTCTCCCGGTATCAGCGCTTCCTCATTTTGA 295
Qy 121 ATCCGCGCTCCGCGTCTTGGCGTCAAGCAGCGGAGAAAGCTGTTTGCAATTTAA 180
Db 296 ATCCGCGCTCCGCGGTCTTGGCGTCAAGCAGCGGAGAAAGCTGTTTGCAATTTAA 355
Qy 181 GCGGCTGTGAACGCCAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 356 GCGGCTGTGAACGCCAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 415
Qy 241 GAGGCGCTTCCAGGAGGCTATTAAGTGAACGCGCGGCGGAGCGGCGGCGGCTTGC 300
Db 416 GAGGCGCTTCCAGGAGGCTATTAAGTGAACGCGCGGCGGAGCGGCGGCGGCTTGC 475
Qy 301 AGGTACTGTAGC-AGACTTCTTTTGTCTTCTTCTTGGGCACTCTGACTGAC 359
Db 476 AGGTACTGTAGCAGGAGCTTCTTTTGTCTTCTTCTTGGGCACTCTGACTGAC 535
Qy 360 TCCCGAGATGAAGCGCTGAGCCGCGGCTGCTGAGAGCGGCTGCTGCTGCT 419
Db 536 TCCCGAGATGAAGCGCTGAGCCGCGGCTGCTGAGAGCGGCTGCTGCTGCTGCT 595
Qy 420 CGGAACGAGTGTGCAATCGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 479
Db 596 CGGAACGAGTGTGCAATCGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 655
Qy 480 TGAGCTTGTGACGACATGAACCACTGCTATCCGCGCTGCGGAACTGTATCCCGAG 539
Db 656 TGAGCTTGTGACGACATGAACCACTGCTATCCGCGCTGCGGAACTGTATCCCGAG 715
Qy 540 TCCCGAGGAGCACTAGCTTGAAGCGAGTGAATCTTACAGCGGCTCATGACTATTC 599
Db 716 TCCCGAGGAGCACTAGCTTGAAGCGAGTGAATCTTACAGCGGCTCATGACTATTC 775
Qy 600 TCGACCTGAGGTATCTCTGCGGAGCGAGCCGCTGAGCCGCTGATGAGCCGCACTTC 659
Db 776 TCGACCTGAGGTATCTCTGCGGAGCGAGCCGCTGAGCCGCTGATGAGCCGCACTTC 835
Qy 660 CCATCCAGACAGCCGAGCTGCTCCGGAATTTGATCTCAACGACAAAGAGACTTTT 719
Db 836 CCATCCAGACAGCCGAGCTGCTCCGGAATTTGATCTCAACGACAAAGAGACTTTT 895
Qy 720 GCGACTGACTGGCGGCTGTCTGACACTCCAGAAAGCAGAGTGTGCGGCCGCTTCTGCC 779
Db 896 GCGACTGACTGGCGGCTGTCTGACACTCCAGAAAGCAGAGTGTGCGGCCGCTTCTGCC 955
Qy 780 TGGGAGCCCGGGAACCTCTCTGCGGAAAGCGGAGCGGAGGAGGAGGAGGAGGAGG 839
Db 956 TGGGAGCCCGGGAACCTCTCTGCGGAAAGCGGAGCGGAGGAGGAGGAGGAGGAGG 1015
Qy 840 CCTGCGCACTTGAACCAATCCCTTCTGAGAGCTTAAACCTGCTCTGAGAGCGGA 899
Db 1016 CCTGCGCACTTGAACCAATCCCTTCTGAGAGCTTAAACCTGCTCTGAGAGCGGA 1075
Qy 900 AGGACTGTGAATTTGAGCTTGAAGAGCAGAGCTTGGCCACAGCTGGGCGAGG 959
Db 1076 AGGACTGTGAATTTGAGCTTGAAGAGCAGAGCTTGGCCACAGCTGGGCGAGG 1135
Qy 960 TCACCTGTGTCACACCCCAAGTTCTAAGTCTTTTCAAGAGCTGAGAGTGTGGA 1019
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Accession	Sequence	Position
Db	1136 TACCCCTGCTCCCAACCCCAACCCCAAGTTCTTCAAGTCGTGAGGCGTGTGGA	1139
QY	1020 AGGAGTGGCTGCTCTTCCAAACTATGACCAGGCGCGGAGAGCTGCTCTTCGTCCT	1079
Db	1196 AGGATGGCTGCTCTCCCAACTATGCCAAGGCGGCGAGAGCTGCTCTTCGGTCTCCT	1255
QY	1080 TGGAGAAAGTCTCTTCCCTCGATTTATGAACTATAAAG-CTAATAGCTTTGTA	1138
Db	1256 TGGAGAAAGTCTCTTCCCTCGATTTATGAACTATAAAGATATAAGCTTTGTA	1315
QY	1139 CCTTTTACACGGAGAGGTGACTTTCTGTAAACAATGCGATATATTAACCTTTTATAA	1198
Db	1316 CCTTTTTCAC-GGAAGGTGACTTTCTGTAAACAATGCGATATATTAACCTTTTATAA	1374
QY	1199 AAGTT 1203	
Db	1375 AAGTT 1379	

RESULT 4  
US-10-084-817-263

```

? Sequence 263, Application US/10084817
? Publication No. US20030119009A1
? GENERAL INFORMATION:
? APPLICANT: Susan Stuart
? APPLICANT: ved G. Nuchtern
? APPLICANT: Sharon E. Plon
? APPLICANT: Jason M. Shohet
? TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
? FILE REFERENCE: PA-0046 US
? CURRENT APPLICATION NUMBER: US/10/084,817
? PRIORITY FILING DATE: 2002-02-23
? PRIOR APPLICATION NUMBER: 60/270,784
? PRIOR FILING DATE: 2001-02-23
? NUMBER OF SEQ ID NOS: 365
? SOFTWARE: PERL Program
? SEQ ID NO 263
? LENGTH: 2066
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc feature
? OTHER INFORMATION: Incyte ID No. US20030119009A1 253987.19
? NAME/KEY: unsure
? LOCATION: 78, 112, 132, 148, 150, 157, 1405
? OTHER INFORMATION: a, t, c, g, or other
? US-10-084-817-263

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Query Match	96.8%	Score 1164.2;	DB 15;	Length 2066;
Best Local Similarity	99.5%;	Pred. No. 0;		
Matches 1199; Conservative	0;	Mismatches 3;	Indels 3.	Gene 3

QY	1	GATCTGGGGTGTCTGCCAGGAAAAACAATTTCTGAAGTTAAATGGTTTGAAGATCTT	60
Db	176	GATCTGGGGTGTCTGCCAGGAAAAACAATTTCTGAAGTTAAATGGTTTGAAGATTTT	235
QY	61	AAATCTTGTCTGGCGGAGAGCCGCGCTCTCCCGGATATAGGGCTTCTCAATCTTTGA	120
Db	236	AAATCTTGTCTGGCGGAGAGCCGCGCTCTCCCGGATATAGGGCTTCTCAATCTTTGA	295
QY	121	ATCCGGCGGCTCCGCGGCTCTTGGGGTCAAGACCAAGCCGAGAGAGCTGTTTCAATTTAA	180
Db	296	ATCCGGCGGCTCCGCGGCTCTTGGGGTCAAGACCAAGCCGAGAGAGCTGTTTCAATTTAA	355
QY	181	GCGGGCTGTGAACGCCACGAGCCGAGCGGGGGCGGAGCGGGCCATTTTGAATAAA	240
Db	356	GCGGGCTGTGAACGCCACGAGCCGAGCGGGGGCGGAGCGGGCCATTTTGAATAAA	415
QY	241	GAGGCGTGGCTTCCAGGCGAGGCTCTAATAATGACCGCGCGGAGCGTGGCGCGCTTGC	300
Db	416	GAGGCGTGGCTTCCAGGCGAGGCTCTAATAATGACCGCGCGGAGCGTGGCGCGCTTGC	475

QY	301	AGGCACTGTAAGC -GGA	CTTTTGGTTTCTTTCTCTTTGGGGCACTCTGGA	CTAC	359
Db	476	AGGCACTGTAAGCGGGAC	CTTTTGGTTTCTTTCTCTTTGGGGCACTCTGGA	CTAC	535
QY	360	TCGCCAGCATGAAGGCGCTGAGC	CCGGTGGCGGCGTCAACGAGGGGGTGTGTGCTGT		419
Db	536	TCGCCAGCATGAAGGGGCGTGA	GCCCGGTGGCGGCTGTCAAGAGCGGTGTGTGCTGT		595
QY	420	CGAAGCGCAATCTGGCCAT	TGCCCCGGGGCCGAGGGAGGGCCCGGACGCTGAGAGCCGC		479
Db	596	CGAAGCGCAATCTGGCCAT	TGCCCCGGGGCCGAGGGAGGGCCCGGACGCTGAGAGCCGC		655
QY	480	TGAGCTTGTGAGCAGCATGAAC	CACTGCTACCTCCCGCTGGGGGAACTGTATCCCGAG		539
Db	656	TGAGCTTGTGAGCAGCATGAAC	CACTGCTACCTCCCGCTGGGGGAACTGTATCCCGAG		715
QY	540	TCGCCGAGGCACTCAGCTT	TAAGCCAGGTGAAATCTTACAGCGCGTCACTGACTATTC		599
Db	716	TCGCCGAGGCACTCAGCTT	TAAGCCAGGTGAAATCTTACAGCGCGTCACTGACTATTC		775
QY	600	TCGACCTGAGAGTAAGCTCG	GGCGGAGCCGACCCCTGTATGACCCCTTGC		659
Db	776	TCGACCTGAGAGTAAGCTCG	GGCGGAGCCGACCCCTGTATGACCCCTTGC		835
QY	660	CCATCCAGACAGCCGAGCT	CGCTCCGGAATTTGTATCTCCACACAAAGAGACTTTT		719
Db	836	CCATCCAGACAGCCGAGCT	CGCTCCGGAATTTGTATCTCCACACAAAGAGACTTTT		895
QY	720	GSCACGACTGGGCGGTCCT	CGAACCCTTCAGAAACGAGGTGCTGGCGCCGTTTGCC		779
Db	896	GSCACGACTGGGCGGTCCT	CGAACCCTTCAGAAACGAGGTGCTGGCGCCGTTTGCC		955
QY	780	TGGGACCCCGGGAACCTT	CTCTGTCGGAAGCCGGAACGGCAGAGGATGGGCCCACTTGC		839
Db	956	TGGGACCCCGGGAACCTT	CTCTGTCGGAAGCCGGAACGGCAGAGGATGGGCCCACTTGC		1015
QY	840	CCTGGCCACTTGA	CTTCAACCAATTCCTTCTTGAGACTAAACCTGTGCTCAGAGCGA		899
Db	1016	CCTGGCCACTTGA	CTTCAACCAATTCCTTCTTGAGACTAAACCTGTGCTCAGAGCGA		1075
QY	900	AGGACTGTGAAC	TTGTAGCTGAAGAGCCAGAGCTAGCTCTGGCCACACAGCTGGGCGACG		959
Db	1076	AGGACTGTGAAC	TTGTAGCTGAAGAGCCAGAGCTAGCTCTGGCCACACAGCTGGGCGACG		1135
QY	960	TCACCCGTCGCCAC	CCCCCAAGTTCTTAAAGTCTTTTCAAGGCTGAGAGGTGTGA		1019
Db	1136	TCACCCGTCGCCAC	CCCCCAAGTTCTTAAAGTCTTTTCAAGGCTGAGAGGTGTGA		1195
QY	1020	AGGAGTGAGTGTCTTCC	AACTAATGACCAAGCGCGGCAAGAGCTGTCTGTCTCT		1079
Db	1196	AGGAGTGAGTGTCTTCC	AACTAATGACCAAGCGCGGCAAGAGCTGTCTGTCTCT		1255
QY	1080	TGGAGAAAGTTCTGT	TGCCCTGATTTAAGACTTAATAAG -GTATAAGGTTTTGTA		1138
Db	1256	TGGAGAAAGTTCTGT	TGCCCTGATTTAAGACTTAATAAG -GTATAAGGTTTTGTA		1315
QY	1139	CCTTTTAAAGGAGAG	GTGACTTCTGTGAACAATCGATGTATATTAACCTTTTATAA		1198
Db	1316	CCTTTTAAAGGAGAG	GTGACTTCTGTGAACAATCGATGTATATTAACCTTTTATAA		1374
QY	1199	AAAGTT 1203			
Db	1375	AAAGTT 1379			

RESULT 5  
US-09-925-298-39  
! Sequence 39, Application US/09925298  
! Publication No. US20020039764#1  
! GENERAL INFORMATION:  
! APPLICANT: Rosen et al.  
! TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
! FILE REFERENCE: PA103

QY	1	GATCTGGGGTGTCTGCACGAAAAAACAATTTCTGAAAGTTAATGGTTTGAATGATCTTT	60
Db	31	GATCTGGGGTGTCTGCACGAAAAAACAATTTCTGAAAGTTAATGGTTTGAATGATTTT	90
QY	61	AAATCTTGTCTGGACGAGAGGCGCGCTCTCCCGGTATCAGCGCTTCTCATTTCTTGA	120
Db	91	AAATCTTGTCTGGACGAGAGGCGCGCTCTCCCGGTATCAGCGCTTCTCATTTCTTGA	150
QY	121	ATCCGCGGCTCCGCGGCTCTTGGAGCGTCAAGCCGAGGAAAGCTGTGTTGCAATTAA	180
Db	151	ATCCCGGCTCCGCGGCTCTTGGAGCGTCAAGCCGAGGAAAGCTGTGTTGCAATTAA	210
QY	181	GGGGGCTGGAAACGCCGAGGGCGGGGGGGGGGGCGAGGCGGGCCATTTTGAATAA	240
Db	211	GCGGGCTGGAAACGCCGAGGGCGGGGGGGGGGGCGAGGCGGGCCATTTTGAATAA	270
QY	241	GAGGCGTGCTTTCAGAGCAGGCTATAATGACCGCGCGGCGAGCGTGGCGCGCTTGC	300
Db	271	GAGGCGTGCTTTCAGAGCAGGCTATAATGACCGCGCGGCGAGCGTGGCGCGCTTGC	330
QY	301	AGGTCACTGTAC -GACTTCTTTTGGTTTTCTTTCTCTTTGGGGGACCTCTGACTAC	359
Db	331	AGGTCACTGTACAGGACTCTTTTGGTTTTCTTTCTCTTTGGGGGACCTCTGACTAC	390
QY	360	TCCGAGCATGAAGGCGTGAAGCCCGGTCGCGGCTGTACAGAGGCGGTCTGCTGT	419
Db	391	TCCGAGCATGAAGGCGTGAAGCCCGGTCGCGGCTGTACAGAGGCGGTCTGCTGT	450
QY	420	CGGAACGCATTTGGCCATCGCCCGGGGCGAGAGGAAGGCGCGGACTGAGAGCGGC	479
Db	451	CGGAACGCATTTGGCCATCGCCCGGGGCGAGAGGAAGGCGCGGACTGAGAGCGGC	510
QY	480	TGAGCTTGTGAGCGACATGAACCACTGTACTCCCGGCTGGGGGAACTGGTAACCGGAG	539
Db	511	TGAGCTTGTGAGCGACATGAACCACTGTACTCCCGGCTGGGGGAACTGGTAACCGGAG	570
QY	540	TCCGAGAGCACTCAGCTTAAGCCAGGTGAAATCTTAAGCGCGCTCATGACTACATTC	599
Db	571	TCCGAGAGCACTCAGCTTAAGCCAGGTGAAATCTTAAGCGCGCTCATGACTACATTC	630
QY	600	TGACACTGAGATGACTCTGGCGGAGCCAGGCCCTGGAACCCCTGATGGCCCCCACTTC	659
Db	631	TGACACTGAGATGACTCTGGCGGAGCCAGGCCCTGGAACCCCTGATGGCCCCCACTTC	690
QY	660	CCATCCAGACGCGGAGCTCGCTCCGGAATCTGTCTTCCAAAGCAAAAGAGCTTTT	719

```

US-10-102-806-39
RESULT 6
Sequence 39, Application US/10102806
Publication No. US20030054421A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Protein
FILE REFERENCE: PA103PCI
CURRENT APPLICATION NUMBER: US/10/102, 806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
LENGTH: 1300
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (641)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (1297)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (1298)
OTHER INFORMATION: n equals a,t,g, or c
US-10-102-806-39

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Query Match 96.7%; Score 1162.8; DB 14; Length 1300;  
 Best Local Similarity 99.1%; Pred. No. 0;  
 Matches 1194; Conservative 5; Mismatches 3; Indels 3; Gaps 3;

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QY 1 GATCTGGGATGCTGTCAGAGAAAAGCAAAATCTGGAAGTAAATGTTTGAAGTAACTT 60
DB 31 GATCTGGGATGCTGTCAGAGAAAAGCAAAATCTGGAAGTAAATGTTTGAAGTAACTT 90
QY 61 AAATCTGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 91 AAATCTGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 150
QY 121 ATCCGCGGCTCCGCGGCTCTTGGGCTGAGACACGCGGAGAGAGAGAGAGAGAGAG 180
DB 151 ATCCGCGGCTCCGCGGCTCTTGGGCTGAGACACGCGGAGAGAGAGAGAGAGAGAG 210
QY 181 GCGGAGCTGTAAAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 211 GCGGAGCTGTAAAGCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 270
QY 241 GAGGCTGCTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 271 GAGGCTGCTCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 330
QY 301 AGGCTCACTGAGC-GGACTTTTGGTTTCTTTCTTTTGGGAGCACTTGAAGTAC 359
DB 331 AGGCTCACTGAGC-GGACTTTTGGTTTCTTTCTTTTGGGAGCACTTGAAGTAC 390
QY 360 TCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
DB 391 TCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 450
QY 420 CGAAGCAGAGTGGCCATGCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 479
DB 451 CGAAGCAGAGTGGCCATGCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 510
QY 480 TGAAGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 539
DB 511 TGAAGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 570
QY 540 TCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 599
DB 571 TCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 630
QY 600 TGAAGCTGAGAGTGGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 659
DB 631 TGAAGCTGAGAGTGGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 690
QY 660 CCATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 719
DB 691 CCATCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 750
QY 720 GCGACTGAGTGGGCGGTGTCTGACACCTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 779
DB 751 GCGACTGAGTGGGCGGTGTCTGACACCTCCAGAGAGAGAGAGAGAGAGAGAGAGAG 810
QY 780 TGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 839
DB 811 TGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 870
QY 840 CCTGCGCACTTGAATTCCTTCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 899
DB 871 CCTGCGCACTTGAATTCCTTCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 930
QY 900 AGGAGTGTGAATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 959
DB 931 AGGAGTGTGAATCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 990
QY 960 TCACCTGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1019
DB 991 TCACCTGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1050

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QY 1020 AGAGTGGCTGCTCCAACTATGCGAAGGCGGCGAGAGCTGCTTTGCTTCTT 1079
DB 1051 AGAGTGGCTGCTCCAACTATGCGAAGGCGGCGAGAGCTGCTTTGCTTCTT 1110
QY 1080 TGAAGAAAGTTCGTTGCTCCCTGATTAATGAAGTCTAATAG-GTAAATAGTTTGT 1138
DB 1111 TGAAGAAAGTTCGTTGCTCCCTGATTAATGAAGTCTAATAGAGTAAATAGTTTGT 1170
QY 1139 CTTTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1198
DB 1171 CTTTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1229
QY 1199 AAGTT 1203
DB 1230 AAGTT 1234

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RESULT 7
US-10-198-846-13483
; Sequence 13483, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinhilber, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198, 846
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306, 220
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13483
; LENGTH: 1504
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1497, 1498, 1499, 1500, 1501, 1502, 1503, 1504
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13483

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Query Match 79.0%; Score 950.8; DB 14; Length 1504;  
 Best Local Similarity 97.4%; Pred. No. 7; 5e-294;  
 Matches 1009; Conservative 0; Mismatches 22; Indels 5; Gaps 4;

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QY 170 TTGCAATTTAAAGGCGGTGTGAAGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAG 229
DB 11 TTGCAATTTAAAGGCGGTGTGAAGCCCGAGAGAGAGAGAGAGAGAGAGAGAGAG 70
QY 230 TTTTGAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 289
DB 71 TTTTGAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 128
QY 290 GCGGCGGTGGAGAGTCACTGTAAGC-GGACTTTTGGTTTCTTTCTTTTGGGAGAG 348
DB 129 GCGGCGGTGGAGAGTCACTGTAAGC-GGACTTTTGGTTTCTTTCTTTTGGGAGAG 188
QY 349 TCTGAGTCACTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 408
DB 189 TCTGAGTCACTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 248
QY 409 GTGCTGCTGTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 468
DB 249 GTGCTGCTGTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 308
QY 469 TGAAGAGCGGTGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 528
DB 309 TGAAGAGCGGTGAGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 368

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QY 529 GGTACCCGGAGTCCCGAGAGGCACTCAGCTTAGCCAGTGAATCTCAAGGCGTCAT 588
|
|
|
Db 369 GGTACCCGGAGTCCCGAGAGGCACTCAGCTTAGCCAGTGAATCTCAAGGCGTCAT 428
|
|
|
QY 589 GCACTACATCTTCGACCTCAGTAGTCTTGCCGAGCCAGCCCTTGAGCCCCCTGATG 648
|
|
|
Db 429 CCACTACATCTTCGACCTCAGTAGTCTTGCCGAGCCAGCCCTTGAGCCCCCTGATG 488
|
|
|
QY 649 CCCCCCACTTCCCATCAACAGCCGAGCTCGTCCGGAATTGTATCTCAACAGCAA 708
|
|
|
Db 489 CCCCCCACTTCCCATCAACAGCCGAGCTCGTCCGGAATTGTATCTCAACAGCAA 548
|
|
|
QY 709 AAGAGCTTTTGCACTGACTGCGCCGTGTCGACCACTCCAGAGCGAGGCTGCGG 768
|
|
|
Db 549 AAGAGCTTTTGCACTGACTGCGCCGTGTCGACCACTCCAGAGCGAGGCTGCGG 608
|
|
|
QY 769 CCGGTTCTGCTGGGACCCCGGGAACCTCTCTGCGGAAGCCGAGCGAGGATGAGC 828
|
|
|
Db 609 CCGGTTCTGCTGGGACCCCGGGAACCTCTCTGCGGAAGCCGAGCGAGGATGAGC 668
|
|
|
QY 829 CCGCACTTGGCCCTGCGCCACTTGACTTACCAATCCCTTCTGAGACTAACTGTG 888
|
|
|
Db 669 CCGCACTTGGCCCTGCGCCACTTGACTTACCAATCCCTTCTGAGACTAACTGTG 728
|
|
|
QY 889 CTCAGAGCGAAGACTGTGAACTTGAGCTGGAAGGCGAGGCTAGCTGCGGACCA 948
|
|
|
Db 729 CTCAGAGCGAAGACTGTGAACTTGAGCTGGAAGGCGAGGCTAGCTGCGGACCA 788
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|
|
QY 949 GCTGGGCGACGTACCCCTGCTCCACCCCAAGTCTTAAGTCTTTTCAGAGCGT 1008
|
|
|
Db 789 GCTGGGCGACGTACCCCTGCTCCACCCCAAGTCTTAAGTCTTTTCAGAGCGT 848
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|
|
QY 1009 GGAAGTGTGAAGAGAGTGGCTGCTCCAACTATGCCAAGCGCGGAGAGCTGTCT 1068
|
|
|
Db 849 GGAAGTGTGAAGAGAGTGGCTGCTCCAACTATGCCAAGCGCGGAGAGCTGTCT 908
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|
|
QY 1069 TCTGGCTCTTGGAGAAAGTTCGTGCTGCTGATTAATGAATCTTAATAG-CTAA 1127
|
|
|
Db 909 TCTGGCTCTTGGAGAAAGTTCGTGCTGCTGATTAATGAATCTTAATAGAGTAA 968
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|
|
QY 1128 TAGGTTTGTACCTTTTTCACAGGAGGTGACTTCTGTAACTGCGATTAATTAA 1187
|
|
|
Db 969 TAGGTTTGTACCTTTTTCAC- GGAAGGTGACTTCTGTAACTGCGATTAATTAA 1027
|
|
|
QY 1188 ACTTTTATATAAGTT 1203
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|
|
Db 1028 ACTTTTATATAAGTT 1043
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|
RESULT 8
US-10-450-826-21
; Sequence 21, Application US/10450826
; Publication No. US20040101818A1
; GENERAL INFORMATION:
; APPLICANT: Ji, Darren
; APPLICANT: Axelrod, Douglas W.
; APPLICANT: Cook, Jonathan S.
; APPLICANT: Jaiswal, Neelam
; APPLICANT: Eistein, Richard
; APPLICANT: Houghton, Adam
; APPLICANT: Metz, Lawrence
; TITLE OF INVENTION: Gene Expression Profiles Associated with Osteoblast Differentiat
; FILE REFERENCE: 044921-5039-WO
; CURRENT APPLICATION NUMBER: US/10/450,826
; PRIOR FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/255,882
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/285,691
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
```

```

; LENGTH: 982
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; INFORMATION: Genbank Accession No. X66924
US-10-450-826-21

Query Match
Best Local Similarity 97.7%; Pred. No. 14e-263;
Matches 900; Conservative 0; Mismatches 18; Indels 3; Gaps 3;

QY 284 GAGCGTGGCGCGGTTCAGAGTCACTGTAGCCGACTTCTTTGTTTCTTTCTTTGG 343
|
|
|
Db 40 GATCTGCAACACCGGAACTCAAGACACTACTTCTTTGTTTCTTTCTTTGG 99
|
|
|
QY 344 GCACTCTTGAGTCACTCCCAAGCATGAAGCGCTGAGCCGCTGCGCGCTGCTAG 403
|
|
|
Db 100 GCACTCTTGAGTCACTCCCAAGCATGAAGCGCTGAGCCGCTGCGCGCTGCTAG 159
|
|
|
QY 404 GCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 463
|
|
|
Db 160 GCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 219
|
|
|
QY 464 GCACTGAGAGCGCGCTGAGCTTGTGAGCATGAACACTGCTACTCCGCTGCGG 523
|
|
|
Db 220 GCACTGAGAGCGCGCTGAGCTTGTGAGCATGAACACTGCTACTCCGCTGCGG 279
|
|
|
QY 524 GAATCTGTACCCGAGAGTCCGAGAGCACTCACTTGAAGCAAGTGAATCTTACAG 583
|
|
|
Db 280 GAATCTGTACCCGAGAGTCCGAGAGCACTCACTTGAAGCAAGTGAATCTTACAG 339
|
|
|
QY 584 GTATCTGACTACTTCTGACTGAGTGTCTGAGAGTGTCTGAGAGCCGCTTGAAG 643
|
|
|
Db 340 GTATCTGACTACTTCTGACTGAGTGTCTGAGAGTGTCTGAGAGCCGCTTGAAG 399
|
|
|
QY 644 GATGCCCCCACTTCCCATCCAGACAGCCGAGTCTGCTCCGGAATTGTCTTCAAC 703
|
|
|
Db 400 GATGCCCCCACTTCCCATCCAGACAGCCGAGTCTGCTCCGGAATTGTCTTCAAC 459
|
|
|
QY 704 GACAAAGAGAGCTTTTGCCTGACTGAGTGTCTGAGCACTTCAAGAGCAAGTGC 763
|
|
|
Db 460 GACAAAGAGAGCTTTTGCCTGACTGAGTGTCTGAGCACTTCAAGAGCAAGTGC 519
|
|
|
QY 764 TGGCGCCGCTTCTGCTGCTGAGAGCCCGGGAACCTTCTCTGCGGAGCCGGAAG 823
|
|
|
Db 520 TGGCGCCGCTTCTGCTGCTGAGAGCCCGGGAACCTTCTCTGCGGAGCCGGAAG 579
|
|
|
QY 824 TGGGCCCAACTTGGCCCTGAGCCCACTTGACTTCAACCAATCCCTTCTGAGACT 883
|
|
|
Db 580 TGGGCCCAACTTGGCCCTGAGCCCACTTGACTTCAACCAATCCCTTCTGAGACT 639
|
|
|
QY 884 TGTGCTGAGAGCGAGAGCTGTGAAGCTGTGAGCTGTGAAGAGCGAGACTAGTCT 943
|
|
|
Db 640 TGTGCTGAGAGCGAGAGCTGTGAAGCTGTGAGCTGTGAAGAGCGAGACTAGTCT 699
|
|
|
QY 944 CACGAGCTGGGAGAGTCACTCTGCTCCCAACCCCAACCCCAAGTCTTAAGTCTT 1003
|
|
|
Db 700 CACGAGCTGGGAGAGTCACTCTGCTCCCAACCCCAACCCCAAGTCTTAAGTCTT 758
|
|
|
QY 1004 AGCGTGAAGGTGTGAAGAGTGTGCTGCTCAACTATGCGAGAGCGCGAGAGCT 1063
|
|
|
Db 759 AGCGTGAAGGTGTGAAGAGTGTGCTGCTCAACTATGCGAGAGCGCGAGAGCT 818
|
|
|
QY 1064 GGTCTTCTGCTCTCTTGAAGAAAGTCTGTGCTGCTGATTTATGAATCTATATAG 1122
|
|
|
Db 819 GGTCTTCTGCTCTCTTGAAGAAAGTCTGTGCTGCTGATTTATGAATCTATATAG 878
|
|
|
QY 1123 GTATATAGTGTGTGACTTTTTCACAGGAAAGTGAATTTTGTAACTATGATAT 1182
|
|
|
Db 879 GTATATAGTGTGTGACTTTTTCAC- GGAAGGTGACTTCTGTAACTATGATAT 937
|
|
|
QY 1183 ATTAAGTTTATATAAGTT 1203
|
|
|
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Db 938 ATTAACTTTTATTAAGTT 958

RESULT 9  
US-10-450-826-23

/ Sequence 23, Application US/10450826  
/ Publication No. US20040101818A1

/ GENERAL INFORMATION:

/ APPLICANT: J1, Darren

/ APPLICANT: Axelrod, Douglas W.

/ APPLICANT: Cook, Jonathan S.

/ APPLICANT: Jaiswal, Neelam

/ APPLICANT: Eistein, Richard

/ APPLICANT: Houghton, Adam

/ APPLICANT: Mertz, Lawrence

/ TITLE OF INVENTION: Gene Expression Profiles Associated with Osteoblast Differentiat

/ FILE REFERENCE: 044921-5039-NO

/ CURRENT APPLICATION NUMBER: US/10/450,826

/ PRIOR FILING DATE: 2003-06-18

/ PRIOR APPLICATION NUMBER: US 60/255,882

/ PRIOR FILING DATE: 2000-12-18

/ PRIOR APPLICATION NUMBER: US 60/285,691

/ PRIOR FILING DATE: 2001-04-24

/ NUMBER OF SEQ ID NOS: 149

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 23

/ LENGTH: 2481

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ FEATURE:

/ OTHER INFORMATION: Genbank Accession No. X73428

US-10-450-826-23

Query Match 55.2%; Score 663.8; DB 17; Length 2481;  
Best Local Similarity 99.7%; Pred. No. 1.2e-201;  
Matches 665; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATCTGGGCTGCTCCAGGAAAGCAATTCGGAAGTATGTTTGAAGTATCTT 60  
DB 372 GATCTGGGCTGCTCCAGGAAAGCAATTCGGAAGTATGTTTGAAGTATCTT 431  
QY 61 AAATCCTTCTGCGGAGAGAGCCCGCTCTCCCGGTATCAGCGCTTCTCATTTTGA 120  
DB 432 AAATCCTTCTGCGGAGAGAGCCCGCTCTCCCGGTATCAGCGCTTCTCATTTTGA 491  
QY 121 ATCCGCGCTCGCGGTCTTTCGCGTCAACCAAGCCGGAAGAACTGTTTGCATTTTA 180  
DB 492 ATCCGCGCTCGCGGTCTTTCGCGTCAACCAAGCCGGAAGAACTGTTTGCATTTTA 551  
QY 181 GCGGGCTGTAAGAGCCAGGAGCCGCGGGGCGGGGCGAGGCGGGCATTTTGAATTA 240  
DB 552 GCGGGCTGTAAGAGCCAGGAGCCGCGGGGCGGGGCGAGGCGGGCATTTTGAATTA 611  
QY 241 GAGGCGTGCCTTCCAGCAGGCTCTAATAAGTGAACCGCGCGGAGCGTGCAGCGCTTGC 300  
DB 612 GAGGCGTGCCTTCCAGCAGGCTCTAATAAGTGAACCGCGCGGAGCGTGCAGCGCTTGC 671  
QY 301 AGGTCACTGAAGCGACTTTTGGTGTCTTCTTCTTGGGAGCACTTGAATCACT 360  
DB 672 AGGTCACTGAAGCGACTTTTGGTGTCTTCTTCTTGGGAGCACTTGAATCACT 731  
QY 361 CCCAGCATGAAGCGCTGAGCCGCGTGCAGGCTCTAAGAGCGGTGTGCTGCTGTC 420  
DB 732 CCCAGCATGAAGCGCTGAGCCGCGTGCAGGCTCTAAGAGCGGTGTGCTGCTGTC 791  
QY 421 GGAACGAGTCTTGCCCATATCCCGGGGCGAGGAGAAAGGCGCGGAGCTGAGAGCGCTT 480  
DB 792 GGAACGAGTCTTGCCCATATCCCGGGGCGAGGAGAAAGGCGCGGAGCTGAGAGCGCTT 851  
QY 481 GAGCTTCTGAGAGCAATGAACCACTGCTACTCCCGCTGCGGGAACTGTACCCGAGT 540  
DB 852 GAGCTTCTGAGAGCAATGAACCACTGCTACTCCCGCTGCGGGAACTGTACCCGAGT 911

QY 541 CCCAGAGGCACTCAGCTTAGCCAGGTGGAATTCCTACAGCGGCTCATCAGTACTTCT 600  
DB 912 CCCAGAGGCACTCAGCTTAGCCAGGTGGAATTCCTACAGCGGCTCATCAGTACTTCT 971  
QY 601 CGACTTGCAAGTAGTCTTGCGCCGAGCCAGCCCTGAGACCCCTGATGGCCCCCACTTTC 660  
DB 972 CGACTTGCAAGTAGTCTTGCGCCGAGCCAGCCCTGAGACCCCTGATGGCCCCCACTTTC 1031  
QY 661 CATTCAG 667  
DB 1032 CATTCAG 1038

RESULT 10  
US-10-450-826-24/c

/ Sequence 24, Application US/10450826  
/ Publication No. US20040101818A1

/ GENERAL INFORMATION:

/ APPLICANT: J1, Darren

/ APPLICANT: Axelrod, Douglas W.

/ APPLICANT: Cook, Jonathan S.

/ APPLICANT: Jaiswal, Neelam

/ APPLICANT: Eistein, Richard

/ APPLICANT: Houghton, Adam

/ APPLICANT: Mertz, Lawrence

/ TITLE OF INVENTION: Gene Expression Profiles Associated with Osteoblast Differentiat

/ FILE REFERENCE: 044921-5039-NO

/ CURRENT APPLICATION NUMBER: US/10/450,826

/ PRIOR FILING DATE: 2003-06-18

/ PRIOR APPLICATION NUMBER: US 60/255,882

/ PRIOR FILING DATE: 2000-12-18

/ PRIOR APPLICATION NUMBER: US 60/285,691

/ NUMBER OF SEQ ID NOS: 149

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 24

/ LENGTH: 129722

/ TYPE: DNA

/ ORGANISM: Homo sapiens

/ FEATURE:

/ OTHER INFORMATION: Genbank Accession No. AL021154

US-10-450-826-24

Query Match 54.3%; Score 652.8; DB 17; Length 129722;  
Best Local Similarity 99.6%; Pred. No. 2.3e-197;  
Matches 665; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 GATCTGGGCTGCTCCAGGAAAGCAATTCGGAAGTATGTTTGAAGTATCTT 60  
DB 109558 GATCTGGGCTGCTCCAGGAAAGCAATTCGGAAGTATGTTTGAAGTATCTT 109499  
QY 61 AAATCCTTCTGCGGAGAGAGCCCGCTCTCCCGGTATCAGCGCTTCTCATTTTGA 120  
DB 109498 AAATCCTTCTGCGGAGAGAGCCCGCTCTCCCGGTATCAGCGCTTCTCATTTTGA 109439  
QY 121 ATCCGCGCTCGCGGTCTTTCGCGTCAACCAAGCCGGAAGAACTGTTTGCATTTTA 180  
DB 109438 ATCCGCGCTCGCGGTCTTTCGCGTCAACCAAGCCGGAAGAACTGTTTGCATTTTA 109379  
QY 181 GCGGGCTGTAAGAGCCAGGAGCCGCGGGGCGGGGCGAGGCGGGGCATTTTGAATTA 240  
DB 109437 GCGGGCTGTAAGAGCCAGGAGCCGCGGGGCGGGGCGAGGCGGGGCATTTTGAATTA 109319  
QY 241 GAGGCGTGCCTTCCAGCAGGCTCTAATAAGTGAACCGCGCGGAGCGTGCAGCGCTTGC 300  
DB 109318 GAGGCGTGCCTTCCAGCAGGCTCTAATAAGTGAACCGCGCGGAGCGTGCAGCGCTTGC 109259  
QY 301 AGGTCACTGAAGCGACTTTTGGTGTCTTCTTCTTGGGAGCACTTGAATCACT 359  
DB 109258 AGGTCACTGAAGCGACTTTTGGTGTCTTCTTCTTGGGAGCACTTGAATCACT 109199  
QY 360 TCCCAAGCATGAAGCGCTGAGCCGCGTGCAGGCTCTAAGAGCGGTGTGCTGCTGT 419

Db 109198 TCCCCAGATGAAGGCGCTGAGCCCGGCTGCGGCTGCTACGAGGCGGTGCTGCTGT 109139  
Qy 420 CGGAACGCACTTGGCCATTCGCCCCGGGGCCGAGGAAAGGCCCCGGCAGTGAAGAGCCGC 479  
Db 109138 CGGAACGCACTTGGCCATTCGCCCCGGGGCCGAGGAAAGGCCCCGGCAGTGAAGAGCCGC 109079  
Qy 480 TGAGCTGTGAGCAGCATGAACCACTGCTACCCGCTGCGGGAACTGTATCCCGAG 539  
Db 109078 TGAGCTGTGAGCAGCATGAACCACTGCTACCCGCTGCGGGAACTGTATCCCGAG 109019  
Qy 540 TCCCGAGAGCACTGAGCTTACCGAGGTGAATCTCTACAGCGCGTCACTGATTC 599  
Db 109018 TCCCGAGAGCACTGAGCTTACCGAGGTGAATCTCTACAGCGCGTCACTGATTC 108959  
Qy 600 TCGACCTGAGAGTAGTCTCTGGCCGAGCCGCCCCCTTGAGACCCCTGATGCCCCCACTTC 659  
Db 108958 TCGACCTGAGAGTAGTCTCTGGCCGAGCCGCCCCCTTGAGACCCCTGATGCCCCCACTTC 108899  
Qy 660 CCATCCAG 667  
Db 108898 CCATCCAG 108891

## RESULT 11

US-09-919-039-214  
; Sequence 214, Application US/09919039  
; Publication No. US20030108871A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaser, Matthew R.  
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES  
; FILE REFERENCE: PA-0035 US  
; CURRENT APPLICATION NUMBER: US/09/919,039  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 401  
; SOFTWARE: PERL Program  
; SEQ ID NO 214  
; LENGTH: 653  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20030108871A1 253987.16  
US-09-919-039-214

Query Match 36.4%; Score 437.8; DB 10; Length 653;  
Best Local Similarity 97.2%; Pred. No. 2,1e-129;

Matches 456; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 736 TGTCTGACACCTCCAGAACGAGGTGCTGGCGCCCGTTCTGCTGAGACCCCGGAAAC 795  
Db 147 TTTCTCTCCCGCCCGCAGAACGAGGTGCTGGCGCCCGTTCTGCTGAGACCCCGGAAAC 206  
Qy 796 TTTCTCTCCCGCAGAACGAGGTGCTGGCGCCCGTTCTGCTGAGACCCCGGAAAC 855  
Db 207 TTTCTCTCCCGCAGAACGAGGTGCTGGCGCCCGTTCTGCTGAGACCCCGGAAAC 266  
Qy 856 CACCAATCCCTTCTGAGACTAAACCTGTGCTCAGAGGAGAACTGTGAACCTGT 915  
Db 267 CACCAATCCCTTCTGAGACTAAACCTGTGCTCAGAGGAGAACTGTGAACCTGT 326  
Qy 916 AGCTGAGAGCCAGAGCTAGCTTGGCCACCAAGCTGGGCGAGCTCACCTGCTCCAC 975  
Db 327 GGCCTGAGAGCCAGAGCTAGCTTGGCCACCAAGCTGGGCGAGCTCACCTGCTCCAC 386  
Qy 976 CCAACCCCAAGTTCTTAAGGTCTTTTCAGAGCGTGGAGGTGGAAGAGTGTCTCTC 1035  
Db 387 CCAACCCCAAGTTCTTAAGGTCTTTTCAGAGCGTGGAGGTGGAAGAGTGTCTCTC 446  
Qy 1036 CAAATATGCAAGGCGGCGGAGAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1095  
Db 447 CAAATATGCAAGGCGGCGGAGAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 506

Qy 1096 TGCCCTGATTTATGACTCTATTAATAG-GTATATAGTTTTGTACTTTTTTACAGGAA 1154  
Db 507 TGCCCTGATTTATGACTCTATTAATAGATATAGTTTTGTACTTTTTTACAGGAA 566  
Qy 1155 GGTGACTTTCTGTAAACATGCGATGTATTAATCTTTTATTAAGTT 1203  
Db 567 GGTGACTTTCTGTAAACATGCGATGTATTAATCTTTTATTAAGTT 615

## RESULT 12

US-10-116-802-341/c  
; Sequence 341, Application US/10116802  
; Publication No. US20030065157A1  
; GENERAL INFORMATION:  
; APPLICANT: Amy Lasek  
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER  
; FILE REFERENCE: PA-0045 US  
; CURRENT APPLICATION NUMBER: US/10/116,802  
; CURRENT FILING DATE: 2002-04-04  
; PRIOR FILING DATE: 2001-04-04  
; NUMBER OF SEQ ID NOS: 519  
; SOFTWARE: PERL Program  
; SEQ ID NO 341  
; LENGTH: 2066  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 253987.19  
; NAME/KEY: unsure  
; LOCATION: 78, 112, 132, 148, 150, 157, 1405  
; OTHER INFORMATION: a, t, c, g, or other  
US-10-116-802-341

Query Match 36.4%; Score 437.8; DB 14; Length 2066;  
Best Local Similarity 97.2%; Pred. No. 3,5e-129;

Matches 456; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

Qy 736 TGTCTGACACCTCCAGAACGAGGTGCTGGCGCCCGTTCTGCTGAGACCCCGGAAAC 795  
Db 1920 TTTCTCTCCCGCCCGCAGAACGAGGTGCTGGCGCCCGTTCTGCTGAGACCCCGGAAAC 1861  
Qy 796 TTTCTCTCCCGCAGAACGAGGTGCTGGCGCCCGTTCTGCTGAGACCCCGGAAAC 855  
Db 1860 TTTCTCTCCCGCAGAACGAGGTGCTGGCGCCCGTTCTGCTGAGACCCCGGAAAC 1801  
Qy 856 CACCAATCCCTTCTGAGACTAAACCTGTGCTCAGAGGAGAACTGTGAACCTGT 915  
Db 1800 CACCAATCCCTTCTGAGACTAAACCTGTGCTCAGAGGAGAACTGTGAACCTGT 1741  
Qy 916 AGCTGAGAGCCAGAGCTAGCTTGGCCACCAAGCTGGGCGAGCTCACCTGCTCCAC 975  
Db 1740 GGCCTGAGAGCCAGAGCTAGCTTGGCCACCAAGCTGGGCGAGCTCACCTGCTCCAC 1681  
Qy 976 CCACCCCAAGTTCTTAAGGTCTTTTCAGAGCGTGGAGGTGGAAGAGTGTCTCTC 1035  
Db 1680 CCACCCCAAGTTCTTAAGGTCTTTTCAGAGCGTGGAGGTGGAAGAGTGTCTCTC 1621  
Qy 1036 CAAATATGCAAGGCGGCGGAGAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1095  
Db 1620 CAAATATGCAAGGCGGCGGAGAGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1561  
Qy 1096 TGCCCTGATTTATGACTCTATTAATAG-GTATATAGTTTTGTACTTTTTTACAGGAA 1154  
Db 1560 TGCCCTGATTTATGACTCTATTAATAGATATAGTTTTGTACTTTTTTACAGGAA 1501  
Qy 1155 GGTGACTTTCTGTAAACATGCGATGTATTAATCTTTTATTAAGTT 1203  
Db 1500 GGTGACTTTCTGTAAACATGCGATGTATTAATCTTTTATTAAGTT 1452

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RESULT 13
US-10-084-817-263/c
; Sequence 263, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jed G. Muchtern
; APPLICANT: Sharon E. Plon
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL Program
; SEQ ID NO 263
; LENGTH: 2066
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030119009A1 253987.19
; LOCATION: 78, 112, 132, 148, 150, 157, 1405
; OTHER INFORMATION: a, t, c, g, or other
US-10-084-817-263

Query Match      36.4%; Score 437.8; DB 15; Length 2066;
Best Local Similarity 97.2%; Pred. No. 3.5e-129;
Matches 455; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

QY 736 TGTCCTGACACCTCCAGAAAGCAGTGTGCGCCCGCTTCTGCTGGAGCCCGGGAACC 795
DB 1920 TTTCCTCCCCCGCCAGAAAGCAGTGTGCGCCCGCTTCTGCTGGAGCCCGGGAACC 1861
QY 796 TCTCTGCGGGAAGCCGGAAGGAGATGGGCCCACTTGCCCTGCCACTTGACTT 855
DB 1860 TCTCTGCGGGAAGCCGGAAGGAGATGGGCCCACTTGCCCTGCCACTTGACTT 1801
QY 856 CACCAAAATCCCTTCTGAGACTAAACCTGTGCTCAAGAGGAGAACTGTAACTTGT 915
DB 1800 CACCAAAATCCCTTCTGAGACTAAACCTGTGCTCAAGAGGAGAACTGTAACTTGT 1741
QY 916 AGCTTGAAGAGCCAGAGCTAGCTGTGCGCACCAAGCTGGAGCACTCACTCTCCACC 975
DB 1740 GGCCTGAAGAGCCAGAGCTAGCTGTGCGCACCAAGCTGGAGCACTCACTCTCCACC 1681
QY 976 CCAACCCCAAGTTCTAAAGTCTTTTCAAGAGCTGGAGGTGTGAAAGAGTGGCTCTC 1035
DB 1680 CCAACCCCAAGTTCTAAAGTCTTTTCAAGAGCTGGAGGTGTGAAAGAGTGGCTCTC 1621
QY 1036 CAAATCTATGCCAAGCGCGCGAGAGCTGTCTTCTGCTCCCTTGGAGAAAGTTCTGT 1095
DB 1620 CAAATCTATGCCAAGCGCGCGAGAGCTGTCTTCTGCTCCCTTGGAGAAAGTTCTGT 1561
QY 1096 TGCCCTGATTTATGAACTCTATATATAG- GTATATAGTTTGTGACTTTTATACAGGAA 1154
DB 1560 TGCCCTGATTTATGAACTCTATATATAG- GTATATAGTTTGTGACTTTTATACAGGAA 1501
QY 1155 GGTGACTTCTGTATCAATGAGATGATATTAATCTTTTATAAAGTT 1203
DB 1500 GGTGACTTCTGTATCAATGAGATGATATTAATCTTTTATAAAGTT 1452

RESULT 14
US-09-918-995-31450
; Sequence 31450, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
```

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; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31450
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(465)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-31450

Query Match      35.3%; Score 425; DB 10; Length 465;
Best Local Similarity 100.0%; Pred. No. 2.3e-125;
Matches 425; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 347 CCTGTGACTCATCTCCCAAGATGAAGCGCTGAGCCCGGTGCGGCTGCTACGAGCG 406
DB 41 CTTGTGACTCATCTCCCAAGATGAAGCGCTGAGCCCGGTGCGGCTGCTACGAGCG 100
QY 407 GTGTGCTGCTGTGCGAAGCAGTGTGCGCATGCGCCGGGAGCCGAGGAAAGGCGCGCA 466
DB 101 GTGTGCTGCTGTGCGAAGCAGTGTGCGCATGCGCCGGGAGCCGAGGAAAGGCGCGCA 160
QY 467 GCTGAGAGCGCGTGAAGCTTGTGAGCAGCATGAACCACTGTACTCTCCGCTTGGGAA 526
DB 161 GCTGAGAGCGCGTGAAGCTTGTGAGCAGCATGAACCACTGTACTCTCCGCTTGGGAA 220
QY 527 CTGATACCCGAGTCTCCGAGAGGCACTGAGCTTATGACAGTGAATCTTACAGCGCTTC 586
DB 221 CTGATACCCGAGTCTCCGAGAGGCACTGAGCTTATGACAGTGAATCTTACAGCGCTTC 280
QY 587 ATGACTACATTTCTGACCTGAGGTAGTCTTGGCGAGCCAGCCCTTGAACCCCTGAT 646
DB 281 ATGACTACATTTCTGACCTGAGGTAGTCTTGGCGAGCCAGCCCTTGAACCCCTGAT 340
QY 647 GGGCCCCACCTTCCCATCCAGACAGCCGAGCTGCTCCGGAACCTTGTATCTTCAACGAC 706
DB 341 GGGCCCCACCTTCCCATCCAGACAGCCGAGCTGCTCCGGAACCTTGTATCTTCAACGAC 400
QY 707 AAAAGAGCTTTTGCACATGACTCGGCGGTGTCTGACACCTCCAGAAAGCAGGTCTGG 766
DB 401 AAAAGAGCTTTTGCACATGACTCGGCGGTGTCTGACACCTCCAGAAAGCAGGTCTGG 460
QY 767 CGGCC 771
DB 461 CGGCC 465

RESULT 15
US-09-918-995-8760
; Sequence 8760, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8760
; LENGTH: 429
; TYPE: DNA
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ORGANISM: Homo sapiens  
US-09-918-995-8760

Query Match 35.1%; Score 422.6; DB 10; Length 429;  
Best Local Similarity 99.1%; Pred. No. 1.3e-124;  
Matches 425; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	315	GACCTCTTTTGTGTTTCTTTCTTTGCGGCACTTGAGCACTACCTCCCAAGCATGAAG	374
DB	1	GACTTCTTTGTGTTTCTTTCTTTGCGGCACTTGAGCACTACCTCCCAAGCATGAAG	60
QY	375	CGCTAGCCCGGTGCGCGGCTGCTAGAGCGGTGTGCTGCTGTGGAACGACAGTTGG	434
DB	61	CGCTAGCCCGGTGCGCGGCTGCTAGAGCGGTGTGCTGCTGTGGAACGACAGTTGG	120
QY	435	CCATGCCCCGGGGCCGAGGGAAGGGCCCGCAGCTGAGGAGCCGCTGAGCTTGTGGACG	494
DB	121	CCATGCCCCGGGGCCGAGGGAAGGGCCCGCAGCTGAGGAGCCGCTGAGCTTGTGGACG	180
QY	495	ACATGAACCACTGCTACTCCCGGCTGCGGGAACGTGTACCCGGAGTCCCGAGAGGCACTC	554
DB	181	ACATGAACCACTGCTACTCCCGGCTGCGGGAACGTGTACCCGGAGTCCCGAGAGGCACTC	240
QY	555	AGCTTAGCCAGGTGGAATCTCTACAGCGGTCATGCACTTCTCGACTGCAGGTAG	614
DB	241	AGCTTAGCCAGGTGGAATCTCTACAGCGGTCATGCACTTCTCGACTGCAGGTAG	300
QY	615	TCCTGGCCGAGCCAGCCCTTGAGACCCCTTGATGGCCCCCACCCTTCCATCCAGACGCCG	674
DB	301	TCCTGGCCGAGCCAGCCCTTGAGACCCCTTGATGGCCCCCACCCTTCCATCCAGACGCCG	360
QY	675	AGCTGCTCCGGAACTTGTCACTCCAAAGAAAGAGCTTTTGCCACTGACTCGGCC	734
DB	361	AGCTGCTCCGGAACTTGTCACTCCAAAGAAAGAGCTTTTGCCACTGACTCGGCC	420
QY	735	GTGTCTCTGA	743
DB	421	GTGTCTCTGA	429

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Job time : 710.883 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 18, 2004, 15:00:58 ; Search time 4379.17 Seconds  
(without alignments)  
10010.347 Million cell updates/sec

Title: US-09-996-529A-5

Perfect score: 1203  
Sequence: 1 gatctgggggtctgcgcagga.....ttaactttataaagct 1203

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821985908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hic: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gsa1: \*  
9: gb\_gsa2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	865.4	71.9	924	1	AL558926
2	865.4	71.9	933	1	AL541035
3	862.2	71.7	924	3	CR597388
4	862.2	71.7	933	3	CR611504
5	862.2	71.7	944	3	CR615457
6	861.6	71.5	944	5	BX458306
7	860.6	71.5	1162	7	CR455737
8	849.2	70.6	943	4	BM916329
9	840.2	69.8	897	3	CR612668
10	837.6	69.6	901	6	CD105185
11	836.4	69.5	912	5	BQ228009
12	834.4	69.4	962	5	BU146429
13	833.6	69.3	1000	4	BM915798
14	831.2	69.1	1043	5	BQ278726
15	830	68.9	988	1	AL551330
16	829.4	68.5	984	4	BM474363
17	824.4	68.2	1045	4	BM471485
18	820.4	68.1	1020	4	BM541973
19	818.8	67.6	910	4	BM601595
20	812.8	67.6	937	5	BQ942011
21	812.8	67.4	986	4	BM477713
22	811	67.2	898	5	BU161821
23	808.2	67.2	898	5	BU161821
24	808.2	67.2	898	5	BU161821

25	806.8	67.1	954	4	BM553062
26	802.8	66.7	1044	4	BM915317
27	802	66.7	866	1	AL551484
28	802	66.7	1037	4	BM809010
29	801	66.6	1044	4	BM558277
30	799.8	66.5	1065	4	BM423840
31	798.4	66.4	937	5	BQ432408
32	797.6	66.3	1000	4	BM559173
33	796.8	66.2	1003	4	BM541804
34	794.6	66.1	854	5	BU179445
35	787.8	65.5	836	5	BQ673836
36	782	65.0	894	5	BUS08601
37	781.6	65.0	819	4	BG761440
38	780.8	64.9	1053	4	BM477872
39	780.6	64.9	873	6	CD390092
40	779.2	64.8	916	5	BQ681632
41	779.2	64.8	1053	4	BM803498
42	777.4	64.6	1107	4	BM803610
43	776.2	64.5	1090	4	BM541892
44	776	64.5	861	1	AL558925
45	775.6	64.5	985	4	BM557861

#### ALIGNMENTS

RESULT 1  
LOCUS AL558926 924 bp mRNA linear EST 02-APR-2004  
DEFINITION AL558926 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED  
Homo sapiens CDNA clone CSODJ007YA07 5-PRIME, mRNA sequence.

ACCESSION AL558926 GI:46184313  
VERSION AL558926.3  
KEYWORDS EST.  
SOURCE Homo sapiens (human)

#### ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
TITLE Full-length cDNA libraries and normalization  
JOURNAL Unpublished (2001)

COMMENT On Feb 15, 2001 this sequence version replaced gi:31283059.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 EVRY cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime  
end enriched double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
951.r

For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?c=CSODJ007YA07&q=951.r.

#### FEATURES

##### source

1. 924  
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/clone="CSODJ007YA07"  
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/cell\_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"  
/note="1st strand cDNA was primed with a NotI-oligo (dt)  
primer. Five prime end enriched, double-strand cDNA was  
digested with Not I and EcoR V  
sites of the pCMVSPORT 6 vector. Library was normalized."

#### ORIGIN

Query Match 71.9%; Score 865.4; DB 1; Length 924;  
Best Local Similarity 99.7%; Pred. No. 8.4e-225;

	Matches	888;	Conservative	0;	Mismatches	1;	Indels	2;	Gaps	2;
QY	314	GA	CTTCTTTTGGTTTCTTTCTTTCTTTGGGGCACCTCTGAGCTACTCCCGACATGAG	373						
Db	4	G	ACTTCTTTTGGTTTCTTTCTTTTGGGGCACCTCTGAGCTACTCCCGACATGAG	63						
QY	374	G	CGTGAAGCCCGATGGCGCGCTGCTACAGAGCGGTGTGCTGCTGTGGAGCGAGCTG	433						
Db	64	G	CGCTAGACCCCGATGGCGCGCTGCTACAGAGCGGTGTGCTGCTGTGGAGCGAGCTG	123						
QY	434	G	CCATGCGCCCGGGGCGGAGGAGGCGCCGCGACGCTGAGAGACCGCTAGCTTGCTGAC	493						
Db	124	G	CCATGCGCCCGGGGCGGAGGAGGCGCCGCGACGCTGAGAGACCGCTAGCTTGCTGAC	183						
QY	494	G	ATATGAACCACTGCTACTCCGCTGCGGGAACTGGTACC	553						
Db	184	G	ATATGAACCACTGCTACTCCGCTGCGGGAACTGGTACC	243						
QY	554	C	AGCTTAGCCAGGTGGAAATCTGAACAGCGCGCATCGACTACATTCCTGAGACTTGACGTA	613						
Db	244	C	AGCTTAGCCAGGTGGAAATCTGAACAGCGCGCATCGACTACATTCCTGAGACTTGACGTA	303						
QY	614	G	TCTGCGCGAGCCAGCCCTTGAGCCCTGATGGCCCACTTCCATCAGACAGCC	673						
Db	304	G	TCTGCGCGAGCCAGCCCTTGAGCCCTGATGGCCCACTTCCATCAGACAGCC	363						
QY	674	G	AGCTTGCCTCCGGAACCTTGATCATCTCCAAACAAGAGACTTTTGCATGACTGCGC	733						
Db	364	G	AGCTTGCCTCCGGAACCTTGATCATCTCCAAACAAGAGACTTTTGCATGACTGCGC	423						
QY	734	C	GTGTCTGACACCTTCCAGAACGCAAGTGTGCGCCGCTTCTGCTGGAGCCCGGGAA	793						
Db	424	C	GTGTCTGACACCTTCCAGAACGCAAGTGTGCGCCGCTTCTGCTGGAGCCCGGGAA	483						
QY	794	C	CTCTCTCGCGGGAACCGGGAACGGAAGGATGGGCCCACTTGCCTGCCCATTTGAC	853						
Db	484	C	CTCTCTCGCGGGAACCGGGAACGGAAGGATGGGCCCACTTGCCTGCCCATTTGAC	543						
QY	854	T	TACCAAAATCCCTTCTGAGACCTAAACCTGAGTCTCAGAGCGAAAGGACTGTGAACCTT	913						
Db	544	T	TACCAAAATCCCTTCTGAGACCTAAACCTGAGTCTCAGAGCGAAAGGACTGTGAACCTT	603						
QY	914	G	TAGCGTGAAGACGACAGCTAGCTTGGGCCACCAAGCTGGGCGACGTCACCTGCTGCCA	973						
Db	604	G	TAGCGTGAAGACGACAGCTAGCTTGGGCCACCAAGCTGGGCGACGTCACCTGCTGCCA	663						
QY	974	C	CCCAACCCCAAGTCTTAAGTCTTTTCAAGAGGTGAGAGGTGTGGAAGAGTGGCTGCTC	1033						
Db	664	C	CCCAACCCCAAGTCTTAAGTCTTTTCAAGAGGTGAGAGGTGTGGAAGAGTGGCTGCTC	723						
QY	1034	T	CCAAACTTAGCCCAAGCGCGGCGAGAGCTGTTCTGTGCTCTCTTGGAGAAAGTGT	1093						
Db	724	T	CCAAACTTAGCCCAAGCGCGGCGAGAGCTGTTCTGTGCTCTCTTGGAGAAAGTGT	783						
QY	1094	G	TTCGCTCTGATTAATGAACCTTAATAG-GTATTAAGTGTGTGATCTTTTTCACAGG	1152						
Db	784	G	TTCGCTCTGATTAATGAACCTTAATAG-GTATTAAGTGTGTGATCTTTTTCACAGG	842						
QY	1153	A	AGGTGACTTTCGTGAACAATGCGATGTATATAACTTTTATATAAAGTT	1203						
Db	843	A	AGGTGACTTTCGTGAACAATGCGATGTATATAACTTTTATATAAAGTT	893						

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 933)  
 Li, W.-B., Gruber, C.C., Ussase, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 On Feb 15, 2001 this sequence version replaced at\_10544817  
 COMMENT

Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: [seqret@genoscope.cns.fr](mailto:seqret@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primers  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library  
was not normalized. Library was constructed by Life Technologies, a  
division of Invitrogen.  
This sequence belongs to sequence cluster 951.r  
For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?w=CSDBE005A11Q1&c=951.r>.  
Location/Qualifiers  
1..933

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/organism="Homo sapiens"
/mol_type="mRNA"
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/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/notes="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

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Query Match	71.9%	Score 865.4;	DB 1;	Length 933;
Best Local Similarity	99.7%;	Pred. No. 8.4e-225;		
Matches 888;	Conservative 0;	Mismatches 1;	Indels 2;	Gaps 2;

QY	314	GGACCTCTTTTGGTTTTCTTTCTCTTTGGGGACA	CTTGGACCTGACCTGACCTCCAGCATGAG	373
Db	13	GGACTCTTTTGGTTTTCTTTCTCTTTGGGGACCT	CTGGACTGACTCTCCAGCATGAG	72
QY	374	GGGCGTGAACCCCGGTGCGCGGCTGCTGACGAG	GGGTGTGCTTCCGTGCGGAACCGACGCTG	433
Db	73	GGGCTGAACCCCGGTGCGCGGCTGCTGACGAG	GGGTGTGCTTCCGTGCGGAACCGACGCTG	1322
QY	434	GGCATCGCCCGGGCCGAGGGAAGGGCCCGG	CAGCTGAGAGGCGCGTGAACCTTGGGAC	493
Db	133	GGCATCGCCCGGGCCGAGGGAAGGGCCCGG	CAGCTGAGAGGCGCGTGAACCTTGGGAC	1922
QY	494	GACATGAACCACTGCTACTCCCGCTTGGGGA	CTGGTACCTGGAGTCCCGAGAGGCACT	553
Db	193	GACATGAACCACTGCTACTCCCGCTTGGGGA	CTGGTACCTGGAGTCCCGAGAGGCACT	252
QY	554	CAGCTTGAACGAGTGGAAATCTTACAGCGG	GTATGACATCATTTCCGACCTTGGAGTA	613
Db	253	CAGCTTGAACGAGTGGAAATCTTACAGCGG	GTATGACATCATTTCCGACCTTGGAGTA	312
QY	614	GTCTCGGCGGACCGACCCCTTGGACCCCT	TGATGGCCCCCACTTCCCATTCGACAGCC	673
Db	313	GTCTCGGCGGACCGACCCCTTGGACCCCT	TGATGGCCCCCACTTCCCATTCGACAGCC	372
QY	674	GAGCTCGCTCCGGAACCTTGTCACTCCAC	ACGAATAAAGAGCTTTTGGCACTGAC	733
Db	373	GAGCTCGCTCCGGAACCTTGTCACTCCAC	ACGAATAAAGAGCTTTTGGCACTGAC	432
QY	734	CGTGTCTTGACACCTTCAGAACGACAG	GTCTGGCCGCTTCTGCTGGGACCCCGGAA	793
Db	433	CGTGTCTTGACACCTTCAGAACGACAG	GTCTGGCCGCTTCTGCTGGGACCCCGGAA	492
QY	794	CGTGTCTCGGGAACCGGACCGGAGGATGG	GGCCCACTTGGCCTTGGCCCACTTGAC	853
Db	493	CGTGTCTCGGGAACCGGACCGGAGGATGG	GGCCCACTTGGCCTTGGCCCACTTGAC	552



[illegible]

Query Match	Best Local Similarity	Matches	Conservative	Mismatches	Indels	Gaps
71.7%; Score 862.2; DB 3; Length 933;	99.4%; Pred. No. 6,3e-224;	886;	0;	3;	2;	2;
314	GGACTCTTTTGGTTTCTTTCTCTTTGGGCACTTGACCTCCGAGATGAAG	13	GACTCTTTTGGTTTCTTTCTCTTTGGGCACTTGACCTCCGAGATGAAG	72		
374	GCCTGAAGCCCGATGCGGCTGCTCAAGGCGGATGCTGCTGGGGAAGGATCTG	73	GCCTGAAGCCCGATGCGGCTGCTCAAGGCGGATGCTGCTGGGGAAGGATCTG	132		
434	GCCATGCCCGGGGCGGAGGAGGCGGAGCTTGAAGAGCCGCTGAGCTTGAC	133	GCCATGCCCGGGGCGGAGGAGGCGGAGCTTGAAGAGCCGCTGAGCTTGAC	192		
494	GACATGAACCACTGCTACTCCGCGCTCGGGAACTGTAACCCGGAGTCCGAGAGCACT	193	GACATGAACCACTGCTACTCCGCGCTCGGGAACTGTAACCCGGAGTCCGAGAGCACT	252		
554	CAGCTTAGCCAGGTGAATCTTACAGCGGCTCATGACTTACATTTCTGACTTGACAGTA	253	CAGCTTAGCCAGGTGAATCTTACAGCGGCTCATGACTTACATTTCTGACTTGACAGTA	312		
614	GTCCTGGCCAGGCGAGCCCTGGAGCCCTGATGAGGCCCCCACTTCCATCCAGACAGCC	313	GTCCTGGCCAGGCGAGCCCTGGAGCCCTGATGAGGCCCCCACTTCCATCCAGACAGCC	372		
674	GAGCTGCTTCGGAACTTGTCACTCTCCACGACAAAGAGCTTTTGGCACTGACTCGG	733	GAGCTGCTTCGGAACTTGTCACTCTCCACGACAAAGAGCTTTTGGCACTGACTCGG	793		
734	CGGTCTCTGACCTCTCGAGAGCAAGTGTGAGGCGCCGTTCTGCTTGGGAGAGCCCGGAA	793	CGGTCTCTGACCTCTCGAGAGCAAGTGTGAGGCGCCGTTCTGCTTGGGAGAGCCCGGAA	853		
854	TTTACCAAAATCCCTTCTCTGAGAGCTTAACTGCTGCTCAGAGCCGAGAGCTGTGAATT	913	TTTACCAAAATCCCTTCTCTGAGAGCTTAACTGCTGCTCAGAGCCGAGAGCTGTGAATT	973		
914	GTAAGCTGAAGAGCCAGAGCTTGTGAGCAAGCTGAGGAGAGCTACCTGCTGCCA	973	GTAAGCTGAAGAGCCAGAGCTTGTGAGCAAGCTGAGGAGAGCTACCTGCTGCCA	1033		
973	GTGGCTGAAGAGCCAGAGCTTGTGAGCAAGCTGAGGAGAGCTACCTGCTGCCA	1033	GTGGCTGAAGAGCCAGAGCTTGTGAGCAAGCTGAGGAGAGCTACCTGCTGCCA	1093		

QY	974	CCCCACCCCAAGTCTAAGTCTTTTCAGACCGTAGAGTGTGAAAGAGTGCGTCTC	103
Db	673	CCCCACCCCAAGTCTAAGTCTTTTCAGACCGTAGAGTGTGAAAGAGTGCGTCTC	732
QY	1034	TCCAAATATGCGCAAGCGCGCGAGAGCTGTCTTCTGATCTCCCTGGAGAAAGTCTT	109
Db	733	TCCAAATATGCGCAAGCGCGCGAGAGCTGTCTTCTGATCTCCCTGGAGAAAGTCTT	792
QY	1094	GTGGCCCTAATTATGAATCTATATATAG-GATATATAGTTTGTACCTTTTACAGGG	115
Db	793	GTGGCCCTAATTATGAATCTATATATAGAGATATATAGTTTGTACCTTTTACAG-G	851
QY	1153	AAGGTGACTTTCTGTACAACTGCATGTATATTAACCTTTTATTAAGTT	1203
Db	852	AAGGTGACTTTCTGTATACAACTGCATGTATATTAACCTTTTATTAAGTT	902
RESULT 5			
CR615457			
LOCUS			
DEFINITION	CR615457	944 bp	mRNA
ACCESSION	full-length cDNA clone CS0DE01YU19 of Placenta of Homo sapiens		
VERSION	CR615457.1		
KEYWORDS	HTC; CNSUT_cDNA.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.		
JOURNAL	Full-length cDNA libraries and normalization		
REMARK	Unpublished		
REFERENCE	Contact : Feng Liang Email : fliang@life.techn.com URL :		
AUTHORS	http://fulllength.invitrogen.com/Invitrogen Corporation 1600		
TITLE	Faraday Avenue		
JOURNAL	2 (bases 1 to 944)		
COMMENT	Genoscope.		
	Direct Submission		
	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :		
	BP 191 31006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr		
	- Web : www.genoscope.cns.fr)		
	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime		
	end enriched, double-strand cDNA was digested with Not I and cloned		
	into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library		
	was normalized. Library was constructed by Life Technologies, a		
	division of Invitrogen.		
FEATURES	Location/Qualifiers		
Source	1..944		
	/organism="Homo sapiens"		
	/mol_type="RNA"		
	/db_xref="taxon:9606"		
	/clone="CS0DE01YU19"		
	/tissue_type="Placenta"		
	/plasmid="pCMVSPORT_6"		
ORIGIN			
Query Match	71.7%;	Score 862.2;	DB 3;
Best Local Similarity	99.4%;	Pred. No. 6,3e-224;	
Matches	886;	Conservative	0; Mismatches 3; Indels 2; Gaps 2;
QY	314	GGAATCTTTTGGTCTTTCTTTCTTTTGGGGCACTGTGACTCACTCCAGCATGAG	373
Db	8	GGAATCTTTTGGTCTTTCTTTCTTTTGGGGCACTGTGACTCACTCCAGCATGAG	67
QY	374	GGCGTAGCCCGTGGCGGCTGTACAGAGGGGATGGTGGCTGTGCGAAGCATGCTG	433
Db	68	GGCGTAGCCCGTGGCGGCTGTACAGAGGGGATGGTGGCTGTGCGAAGCATGCTG	127
QY	434	GCCATGCCCCGGGGCGAGAGGAGGCGCGGAGCTGAGAGCCGCTGAGCTTGTGAC	493
Db	128	GCCATGCCCCGGGGCGAGAGGAGGCGCGGAGCTGAGAGCCGCTGAGCTTGTGAC	187



QY 1034 TCCAACTATCCAGGCGCGGAGAGCTGTCTTCTGGCTCTTGGAGAAAGTTCT 1093  
DB 728 TCCAACTATCCAGGCGCGGAGAGCTGTCTTCTGGCTCTTGGAGAAAGTTCT 787  
QY 1094 GTTCCCTGATTTTGAAGCTCTATATAG-GTATATAGGTTTGTACCTTTTACAGG 1152  
DB 788 GTTCCCTGATTTTGAAGCTCTATATAGGATATAGTTTGTACCTTTTAC-AG 846  
QY 1153 AAGGTGACTTCTGTACATGAGATGTATATTAACCTTTTAAAGTT 1203  
DB 847 AAGGTGACTTCTGTACATGAGATGTATATTAACCTTTTAAAGTT 897

RESULT 7  
CF455737 1162 bp mRNA linear EST 04-SEP-2003  
LOCUS AGENCOURT 15364529 lupski\_anterior\_horn Homo sapiens cDNA clone  
DEFINITION IMAGE:30515866 5', mRNA sequence.  
ACCESSION CF455737  
VERSION CF455737.1 GI:34455393  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE NIH-MGC http://mgc.nci.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Dr. James R. Lupski  
CDNA Library Preparation: Invitrogen Corp  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
plate: NDAM581 row: k column: 11  
High quality sequence start: 9  
High quality sequence stop: 873.

## FEATURES

source  
Location/Qualifiers  
1..1162  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30515866"  
/issue\_type="Peripheral Nervous system"  
/lab\_host="DH10B (TI phage-resistant)"  
/clone\_lib="lupski anterior horn"  
/note="Vector: pCMV-SPORT6.1; Site 1: EcoRV (destroyed);  
Site 2: NotI; Library is oligo-dT primed and directionally  
cloned (EcoRV site is destroyed upon cloning). Average  
insert size 2.1 kb. Library was constructed by Invitrogen  
and donated by J. Lupski, M.D./Ph.D. (Baylor College of  
Medicine)."

## ORIGIN

Query Match 71.5%; Score 860.6; DB 7; Length 1162;  
Best Local Similarity 99.3%; Pred. No. 1.8e-223;  
Matches 885; Conservative 0; Mismatches 4; Indels 2; Gaps 2;  
QY 314 GGAATCTTTTGGTTCTTTCTTTGGGACCTCGAAGTCCAGAGATGAG 373  
DB 37 GGAATCTTTTGGTTCTTTCTTTGGGACCTCGAAGTCCAGAGATGAG 96  
QY 374 GCGCTGACCCGCGGCGGCTGCTAGAGCGGTGTGCTGCTGCGAAGCGAGTCTG 433  
DB 97 GCGCTGACCCGCGGCGGCTGCTAGAGCGGTGTGCTGCTGCGAAGCGAGTCTG 156

QY 434 GCATCGCCCGGCGCGAGGAGGCGCCGCGACGTAGAGAGCCGCTGAGCTTCTGGAC 493  
DB 157 GCATCGCCCGGCGCGAGGAGGCGCCGCGACGTAGAGAGCCGCTGAGCTTCTGGAC 216  
QY 494 GACATGAACCACTGCTATCCCGGCTGCGGGAATGGTATACCCGAGTCCGAGAGCACT 553  
DB 217 GACATGAACCACTGCTATCCCGGCTGCGGGAATGGTATACCCGAGTCCGAGAGCACT 276  
QY 554 CAGCTTACCGAGTGAATCTCTACAGCGGTCTATGACTATTCCTGACCTGACAGTA 613  
DB 277 CAGCTTACCGAGTGAATCTCTACAGCGGTCTATGACTATTCCTGACCTGACAGTA 336  
QY 614 GTCTGGCGGAGCGACGCCCTTGACCCCTGATAGGCCCACTTCCATCCAGACGCC 673  
DB 337 GTCTGGCGGAGCGACGCCCTTGACCCCTGATAGGCCCACTTCCATCCAGACGCC 396  
QY 674 GAGCTCGCTCCGGAACCTTGTATCTCCAGAGCAAAAGAGCTTTGGCCATCTCGGC 733  
DB 397 GAGCTCACTCCGGAACCTTGTATCTCCAGAGCAAAAGAGCTTTGGCCATCTCGGC 456  
QY 734 GTGTCTGACACCTCCAGAGCGAGGTGTGCGCCGCTTCTGCTGGGACCCCGGAA 793  
DB 457 GTGTCTGACACCTCCAGAGCGAGGTGTGCGCCGCTTCTGCTGGGACCCCGGAA 516  
QY 794 CCTGCTCGCGGAGAGCGGACCGGAGTGGGCCCACTTGGCTGCGCACTTGAC 853  
DB 517 CCTGCTCGCGGAGAGCGGACCGGAGTGGGCCCACTTGGCTGCGCACTTGAC 576  
QY 854 TTACCAAAATCCCTTCTGAGACTAAACCTGCTGCTGAGAGCGAAGAGCTGTAACTT 913  
DB 577 TTACCAAAATCCCTTCTGAGACTAAACCTGCTGCTGAGAGCGAAGAGCTGTAACTT 636  
QY 914 GTAGCTGAAGAGCGCAGAGTCTGTGCGCACAGCTGGGCGACCTGCTGCCA 973  
DB 637 GTAGCTGAAGAGCGCAGAGTCTGTGCGCACAGCTGGGCGACCTGCTGCCA 696  
QY 974 CCCACCCCCCAATTTCTTAAGGTCTTTTCAAGGTGTGAGAGTGTGGAAGAGTGTGCTC 1033  
DB 697 CCCACCCCCCAATTTCTTAAGGTCTTTTCAAGGTGTGAGAGTGTGGAAGAGTGTGCTC 756  
QY 1034 TCCAACTATCCAGGCGCGGAGAGCTGTCTTCTGCTCTGCTGGAAGAAAGTTCT 1093  
DB 757 TCCAACTATCCAGGCGCGGAGAGCTGTCTTCTGCTCTGCTGGAAGAAAGTTCT 816  
QY 1094 GTTCCCTGATTTTGAAGCTCTATATAG-GTATATAGGTTTGTACCTTTTACAGG 1152  
DB 817 GTTCCCTGATTTTGAAGCTCTATATAGGATATAGTTTGTACCTTTTAC-AG 875  
QY 1153 AAGGTGACTTCTGTACATGAGATGTATATTAACCTTTTAAAGTT 1203  
DB 876 AAGGTGACTTCTGTACATGAGATGTATATTAACCTTTTAAAGTT 926

RESULT 8  
BM916329 943 bp mRNA linear EST 12-MAR-2002  
LOCUS AGENCOURT 6641978 NIH\_MGC\_41 Homo sapiens cDNA clone IMAGE:5482718  
DEFINITION 5', mRNA sequence.  
ACCESSION BM916329  
VERSION BM916329.1 GI:19366708  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE NIH-MGC http://mgc.nci.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished (1999)  
Contact: Robert Struhsberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: DCTD/DP  
CDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
 Plate: LNCM2009 row: d column: 15  
 High quality sequence stop: 692.

## FEATURES

source

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 location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5482718"  
 /tissue\_type="amelanotic melanoma, cell line"  
 /lab\_host="PH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_41"  
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
 into EcoRI/XhoI sites using the following 5' adaptor:  
 GGCAGAG(G). Library constructed by Ling Hong in the  
 laboratory of Gerald M. Rubin (University of California,  
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
 Superscript II RT (Life Technologies). Note: this is a  
 NIH\_MGC Library."

## ORIGIN

Query Match 70.6%; Score 849.2; DB 4; Length 943;  
 Best Local Similarity 99.2%; Pred. No. 2.2e-220;  
 Matches 884; Conservative 0; Mismatches 4; Indels 3; Gaps 3;

QY 314 GGAATCTTTTGGTTTCTTTCTTTGGGACCTTGACTCACTCCCGAGATGAAG 373  
 DB 1 GGACTCTTTTGGTTTCTTTCTTTGGG-ACCTTGACTCACTCCCGAGATGAAG 59  
 QY 374 GGGCTAGCCCGGCTGCGGCTGCTACGAGCGGTGTGCTGCTGCGAGACGAGCTG 433  
 DB 60 GGGCTAGCCCGGCTGCGGCTGCTACGAGCGGTGTGCTGCTGCGAGACGAGCTG 119  
 QY 434 GGCATCGCCCGGCGGAGGAGGCGGCACTGAGAGCCGCTGAGCTTGTCTGAC 493  
 DB 120 GGCATCGCCCGGCGGAGGAGGCGGCACTGAGAGCCGCTGAGCTTGTCTGAC 179  
 QY 494 GACATGAACCACTGCTACTCCGCGTGGGGAATGCTACCGGAGTCCCGAGAGCACT 553  
 DB 180 GACATGAACCACTGCTACTCCGCGTGGGGAATGCTACCGGAGTCCCGAGAGCACT 239  
 QY 554 CAGCTTAGCGAGTGAATCTTACAGCGCTCATGCACTACATTTCTGACCTGAGGTA 613  
 DB 240 CAGCTTAGCGAGTGAATCTTACAGCGCTCATGCACTACATTTCTGACCTGAGGTA 299  
 QY 614 GTCTGGCCGAGCCAGCCCTTGAGACCTCTGATGCCCCACCTTCCATCCAGACAGCC 673  
 DB 300 GTCTGGCCGAGCCAGCCCTTGAGACCTCTGATGCCCCACCTTCCATCCAGACAGCC 359  
 QY 674 GAGCTCGCTCGGGAATTGTCACTTCCAGCAAAAGAGGTTTGGACAGTCCGCG 733  
 DB 360 GAGCTCGCTCGGGAATTGTCACTTCCAGCAAAAGAGGTTTGGACAGTCCGCG 419  
 QY 734 CGTGTCTGACACTTCCAGAACGAGTGTGCGCCCTTGTGCTGCGAGCCCGGGA 793  
 DB 420 CGTGTCTGACACTTCCAGAACGAGTGTGCGCCCTTGTGCTGCGAGCCCGGGA 479  
 QY 794 CTTCTCTGCGGGAAGCGGAGCGGATGGGCCCACTTGGCCCTGCGCACTTGAAC 853  
 DB 480 CTTCTCTGCGGGAAGCGGAGCGGATGGGCCCACTTGGCCCTGCGCACTTGAAC 539  
 QY 854 TTCACTCAATCCCTTCTGAGAGCTAACTGTGCTGAGCGAGAGAGCTGTGAATCT 913  
 DB 540 TTCACTCAATCCCTTCTGAGAGCTAACTGTGCTGAGCGAGAGAGCTGTGAATCT 599  
 QY 914 GTAGCTGAAGAGCAGAGCTAGCTTGGCCACAGCTGGGCGAGAGCTGCTGCCA 973  
 DB 600 GTAGCTGAAGAGCAGAGCTAGCTTGGCCACAGCTGGGCGAGAGCTGCTGCCA 659

QY 974 CCCACCCCCAAGTTCTAAGTCTTTTCAGAGCGGTGAGGTGGAAGAGTGTGCTC 1033  
 DB 660 CCCACCCCCAAGTTCTAAGTCTTTTCAGAGCGGTGAGGTGGAAGAGTGTGCTC 719  
 QY 1034 TCCAACTATGCCAAGCGGCGGAGAGCTGTCTTGTGCTCCTTGGAGAAAGTTCT 1093  
 DB 720 TCCAACTATGCCAAGCGGCGGAGAGCTGTCTTGTGCTCCTTGGAGAAAGTTCT 779  
 QY 1094 GTTGCCCTGATTTATGAATCTTAATAG-GTATATAGCTTTTGTACCTTTTACAGCG 1152  
 DB 780 GTTGCCCTGATTTATGAATCTTAATAGTATATAGTATATAGTATTTGACCTTTTACA-GG 838  
 QY 1153 AAGTGACTTTCTGTAACATAGCATGTATTAACCTTTTATAAAGTT 1203  
 DB 839 AAGTGACTTTCTGTAACATAGCATGTATTAACCTTTTATAAAGTT 889

RESULT 9  
 LOCUS CR612668  
 DEFINITION Full-length cDNA clone CS0D1064YG12 of Placenta Cot 25-normalized  
 of Homo sapiens (human).  
 ACCESSION CR612668  
 VERSION CR612668.1 GI:50493475  
 KEYWORDS HTC; CNSLT\_CDNA.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Li M.B., Gruber C., Jessee J. and Polayes P.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: <http://fulllength.invitrogen.com/InvitrogenCorporation1600>  
 Faraday Avenue  
 2 (bases 1 to 897)

REFERENCE  
 AUTHORS Genoscope.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail: [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr))

COMMENT  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen.

## FEATURES

source

1..897  
 location/Qualifiers  
 /organism="Homo sapiens"  
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## ORIGIN

Query Match 69.8%; Score 840.2; DB 3; Length 897;  
 Best Local Similarity 99.4%; Pred. No. 6.3e-218;  
 Matches 864; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 336 TCTTTGGGCACTTGTGACTCACTCCCGAGATGAAGCGCTGAGCCCGTGTGCGGCT 395  
 DB 1 TCTTTGGGCACTTGTGACTCACTCCCGAGATGAAGCGCTGAGCCCGTGTGCGGCT 60  
 QY 396 GCTACGAGCGGATGCTGCTGCGAAGCAGTCTGCGCATCGCCCGGCGGAGGGA 455  
 DB 61 GCTACGAGCGGATGCTGCTGCGAAGCAGTCTGCGCATCGCCCGGCGGAGGGA 120  
 QY 456 AGGCGCGGCACTGAGAGCGGCTGAGCTTGTGAGCAGATGAACCACTGCTACTCC 515  
 DB 121 AGGCGCGGCACTGAGAGCGGCTGAGCTTGTGAGCAGATGAACCACTGCTACTCC 180

QY 516 GCCGAGGGGAACCTGTAACCCGAGTCCCGAGAGCACTACGCTTACGAGTGGAAATCC 575  
Db 181 GCTTCGGGAACCTGTAACCCGAGTCCCGAGAGCACTACGCTTACGAGTGGAAATCC 240  
QY 576 TACAGCGCGTCACTGACATTAATCTGACCTGAGGTAAGTCTGCGGAGCCAGCCCTG 635  
Db 241 TACAGCGCGTCACTGACATTAATCTGACCTGAGGTAAGTCTGCGGAGCCAGCCCTG 300  
QY 636 GACCCCTGATGAGCCCGCACTTCCCATCCAGACAGCCGAGTCTGCGGAACTTGTCA 695  
Db 301 GACCCCTGATGAGCCCGCACTTCCCATCCAGACAGCCGAGTCTGCGGAACTTGTCA 360  
QY 696 TCTCAACGACAAAGAGCTTTGCACTGACCTGAGCGGTCTGACACCTCCAGAAC 755  
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QY 756 GCGAGTCTGAGCCCGCTTCTGCTGAGACCCCGGGAACCTCTCTGCGGAGCCGAGC 815  
Db 421 GCGAGTCTGAGCCCGCTTCTGCTGAGACCCCGGGAACCTCTCTGCGGAGCCGAGC 480  
QY 816 GCGAGGATGAGCCCGCACTTCCCATCCAGACAGCCGAGTCTGCGGAACTTGTCA 875  
Db 481 GCGAGGATGAGCCCGCACTTCCCATCCAGACAGCCGAGTCTGCGGAACTTGTCA 540  
QY 876 ACTAAACCTGAGTCTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 935  
Db 541 ACTAAACCTGAGTCTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
QY 936 GCTCTGAGCCAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 995  
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QY 996 CTTTTCAGAGCGTGAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1055  
Db 661 CTTTTCAGAGCGTGAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720  
QY 1056 GCGAGAGCTGCTTCTGCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1115  
Db 721 GCGAGAGCTGCTTCTGCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
QY 1116 ATAAATG-ATAATGATTTTGTACCTTTTACAGGAGAGAGAGAGAGAGAGAGAG 1174  
Db 781 ATAAATGATTAATGATTTTGTACCTTTTACAGGAGAGAGAGAGAGAGAGAGAG 839  
QY 1175 CGATGATATTAATGATTTTATTAAGTT 1203  
Db 840 CGATGATATTAATGATTTTATTAAGTT 868

RESULT 10  
CD105185 901 bp mRNA linear EST 15-MAY-2003  
LOCUS AGENCOURT 14018727 NIH MGC 179 Homo sapiens cDNA clone  
DEFINITION IMAGE:3036955 5', mRNA sequence.  
ACCESSION CD105185  
VERSION CD105185.1 GI:30758359  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 901)  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Invitrogen Corp  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
Plate: NDAM427 row: F column: 20  
High quality sequence start: 6  
High quality sequence stop: 675.  
Location/Qualifiers  
1..901  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3036955"  
/tissue\_type="placental"  
/lab\_host="DH10B-Ton A (T1 and T5 phage resistance)"  
/clone\_id="NIH\_MGC\_179"  
/note="Organ: brain; Vector: pCMV-Sport6.1; Site 1: Scorey (destroyed); Site 2: NotI; Library is oligo-dT primed and directionally cloned (Scorey site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH MGC library."  
ORIGIN  
Query Match 69.6%; Score 837.6; DB 6; Length 901;  
Best Local Similarity 98.3%; Pred. No. 3,3e-217;  
Matches 857; Conservative 0; Mismatches 14; Indels 1; Gaps 1;  
QY 314 GAACTTTCTTTGGTTTCTTTCTTTGGGACCTCTGACTACTCCAGCATGAAG 373  
Db 30 GAACTTTCTTTGGTTTCTTTCTTTGGGACCTCTGACTACTCCAGCATGAAG 89  
QY 374 GCGCTGAGCCGGGAGCGGCTGCTGAGAGCGGAGTCTGCTGCGAGAGAGAGAGAG 433  
Db 90 GCGCTGAGCCGGGAGCGGCTGCTGAGAGCGGAGTCTGCTGCGAGAGAGAGAGAG 149  
QY 434 GCCATGCCCGGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 493  
Db 150 GCCATGCCCGGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 209  
QY 494 GACATGAACACCTGCTACTCTCCGCTGCGGAACTGTAACCGGAGTCCGAGAGCACT 553  
Db 210 GACATGAACACCTGCTACTCTCCGCTGCGGAACTGTAACCGGAGTCCGAGAGCACT 269  
QY 554 CAGCTTACGAGGATGAAATCTCAACGCGGCTCATGACATCTCGACCTCGACAGTA 613  
Db 270 CAGCTTACGAGGATGAAATCTCAACGCGGCTCATGACATCTCGACCTCGACAGTA 329  
QY 614 GTCTGAGCGAGCGAGCCCTCTGAGATGAGCCCGACCTTCCATCGAGAGCC 673  
Db 330 GTCTGAGCGAGCGAGCCCTCTGAGATGAGCCCGACCTTCCATCGAGAGCC 389  
QY 674 GAGCTGCTCCGGAATTTGTCAATCTCCAGACAAAGAGAGAGAGAGAGAGAGAGAG 733  
Db 390 GAGCTGCTCCGGAATTTGTCAATCTCCAGACAAAGAGAGAGAGAGAGAGAGAGAG 449  
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QY 914 GTAGCTTGAAG 973  
Db 630 GTAGCTTGAAG 689  
QY 974 CCCACCCCGCAAGTTCTAAGGCTTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1033  
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QY 1034 TCCAAACTATGCGAAGGGGGGCGAGAGCTGCTTCTGCTCTCTGGAGAAGGTTCT 1093  
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QY 1094 GTTGCCCTGATTATGAAGCTCTATATAG-GTATATAGTTTGTACCTTTTTCACAGG 1152  
DB 810 GGTGCCCTGATTATGAAGCTCTATATAGATATATAGTTTGTATACCTTTTTCGCGG 869  
QY 1153 AAGTGACTTCTGTAAACATGCGATGTATAT 1184  
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RESULT 11  
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DEFINITION 5', mRNA sequence.  
ACCESSION B0228009  
VERSION B0228009.1 GI:20409409  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 912)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM12875 row: n column: 06  
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/clone="IMAGE:5786693"  
/issue\_type="telomysarcoma"  
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/clone\_lib="NIH\_MGC\_71"  
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Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2.1 kb."

ORIGIN  
Query Match 69.5%; Score 836.4; DB 5; Length 912;  
Best Local Similarity 98.4%; Pred. No. 6.9e-217;  
Matches 876; Conservative 0; Mismatches 11; Indels 3; Gaps 3;

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QY 374 GCGCTGAGCCCGGTCGCGGCTCTACGAGCGGTGTGTGCTGCTCGAAAGCAGTCTG 433  
DB 71 GCGCTGAGCCCGGTCGCGGCTCTACGAGCGGTGTGTGCTGCTCGAAAGCAGTCTG 130  
QY 434 GCCATCGCCCGGCGCGGAGGAGGCGCGGAGCTGAGAGCGCGCTGAGCTTGTGAC 493  
DB 131 GCCATCGCCCGGCGCGGAGGAGGCGCGGAGCTGAGAGCGCGCTGAGCTTGTGAC 190  
QY 494 GACATGAACCACTGCTACTCCGCTGCGGGAACGTGTACCGCGAGTCCCGAGAGCACT 553

DB 191 GACATGAACCACTGCTACTCCGCTGCGGGAAGTGTATACCCGAGTCCCGAGAGCACT 250  
QY 554 CAGCTTAGCCAGGTGGAAATCTTACAGCGCGTCACTGACTATCTTGACCTGAGGTA 613  
DB 251 CAGCTTAGCCAGGTGGAAATCTTACAGCGCGTCACTGACTATCTTGACCTGAGGTA 310  
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DB 311 GTTCGGCGCGAGCGAGCCCTGAGACCCCTGATAGGCCCCCACTTCCATCAGACAGC 370  
QY 674 GAGCTCGCTCCGGAATGTGATCTCAACGACAAAGAGCTTTGCACTGACTCGGC 733  
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QY 734 GTGTCTGACACCTCCAGAAAGCAGGTGCTGGGCGCGCTTCTGCTGGAGCCCGGAA 793  
DB 431 GTGTCTGACACCTCCAGAAAGCAGGTGCTGGGCGCGCTTCTGCTGGAGCCCGGAA 490  
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DB 790 GTTGCCCTGATTATGAAGCTCTATATATAGTATATATAGTTTGTACCTTTTTCACAGGA 847  
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RESULT 12  
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LOCUS AGENCOURT 8725408 NIH\_MGC\_47 Homo sapiens cDNA clone IMAGE:6340250  
DEFINITION 5', mRNA sequence.  
ACCESSION B0146429  
VERSION B0146429.1 GI:22659961  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1 (bases 1 to 962)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LLM2536 row: g column: 03



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High quality sequence stop: 719.  
Location/Qualifiers

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/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 69.4%; Score 834.4; DB 5; Length 962;  
Best Local Similarity 96.8%; Pred. No. 2.5e-216;  
Matches 872; Conservative 0; Mismatches 27; Indels 2; Gaps 2;

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DB 21 GGTCACTGTAGCGGGCTCTTTGGTTTCTTCTTTGGGGACCTCTGGACTACT 80
QY 361 CCCGACATGAAAGGCGCTGAGCCCGGCTGCGCGCTGCTACGAGCGGTGTGCTGCTGTC 420
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QY 421 GGAAGCGAGTCTGGCCATGCTCCCGGCGCGAGGAGGCGCGCGACCTGAGAGCGGCT 480
DB 141 GGAAGCGAGTCTGGCCATGCTCCCGGCGCGAGGAGGCGCGCGACCTGAGAGCGGCT 200
QY 481 GAGCTTGTGAGCAGATGAAACCACTGCTACCTCCGCTCGGGGAACTGTATCCCGGAGT 540
DB 201 GAGCTTGTGAGCAGATGAAACCACTGCTACCTCCGCTCGGGGAACTGTATCCCGGAGT 260
QY 541 CCCGAGGAGCACTGAGCTTGAAGCAGAGGAACTCTAAGCGCGCTCATGCACTAATCT 600
DB 261 CCCGAGGAGCACTGAGCTTGAAGCAGAGGAACTCTAAGCGCGCGCTCATGCACTAATCT 320
QY 601 CGAAGCTGAGAGTATGCTGCGCGAGCCAGCCCTTGAACCCCTGATGCGCCCACTTCC 660
DB 321 CGAAGCTGAGAGTATGCTGCGCGAGCCAGCCCTTGAACCCCTGATGCGCCCACTTCC 380
QY 661 CATCCAGACAGCGAGCTGCTCGCGGAACTTGTCTCCAAAGCAAGAAAGAGCTTTTG 720
DB 381 CATCCAGACAGCGAGCTGCTCGCGGAACTTGTCTCCAAAGCAAGAAAGAGAGCTTTTG 440
QY 721 CCAGTACTGCGCGCTGCTCTGACACTTCAGAAAGAGTGTGCGCGCTTGTGCT 780
DB 441 CCAGTACTGCGCGCTGCTCTGACACTTCAGAAAGAGTGTGCGCGCTTGTGCT 500
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DB 501 GGGAGCCCGGGGAACTTCTCTGCGCGGAAAGCGGAGCGGAGGAGGCTCCCACTTGGCC 560
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QY 901 GGAAGTGAATCTTGTAGCTGAGAGCAAGAGTGTGTGCGCAACGAGTGTGAGAGT 960
DB 621 GGAAGTGAATCTTGTAGCTGAGAGCAAGAGTGTGTGCGCAACGAGTGTGAGAGT 680
QY 961 CACCTGTCTCCACCCCAAGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 1020
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QY 1081 GGAAGAAAGTCTCTTCCCGCTGATTTATGAACTATATAGATATA-GGTTTGTAC 1139
DB 801 GGAAGAAAGTCTGATGCTGCTGATTTATGAACTATATAGAGATATAGGTTGTATC 860
QY 1140 CTTTTTACAGGAAAGTGTACTTCTGTAAACAATGCGATGTATATTAACCTTTTATATA 1199
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DB 921 A 921
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## RESULT 13

BM915798 1000 bp mRNA linear EST 12-MAR-2002  
LOCUS AGENCOURT\_6639758 NIH\_MGC\_41 Homo sapiens cDNA clone IMAGE:5482051  
DEFINITION 5', mRNA sequence.  
ACCESSION BM915798  
VERSION BM915798.1 GI:19366177  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgs.nci.nih.gov/  
1 (bases 1 to 1000)  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
COMMENT Email: cgabs-remail.nih.gov  
Contact: Robert Strauberg, Ph.D.  
Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LNCM2007 row: h column: 20  
High quality sequence stop: 642.

## FEATURES

## Source

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/note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 69.3%; Score 833.6; DB 4; Length 1000;  
Best Local Similarity 97.6%; Pred. No. 4.1e-216;  
Matches 867; Conservative 0; Mismatches 19; Indels 2; Gaps 2;

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DB 12 GAGCTTTTGTGTTTCTTCTTCTTGTGGGACCTCTGAGACTACCTCCCAAGATGAA 71
QY 374 GCCTGAGCCGGTGGCGGCTGCTAGAGAGCGGTGTGCTGTCTGCGAAGCAAGTCTG 433
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Db 72 GCGCTGAGCCGGTGGCGGCTGCTACGAGCGGCTGCTGCTGCTGCGAAGCGAGCTG 131  
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Qy 494 GACATGAACCATGCTACTCCGCGCTGCGGAACTGTACTCCGAGTCCCGAGAGGCACT 553  
Db 192 GACATGAACCATGCTACTCCGCGCTGCGGAACTGTACTCCGAGTCCCGAGAGGCACT 251  
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Db 252 GAGCTTACGAGGAGGAACTCTTACAGCGCGCTGATGACTATGCTGACCTGACAGTA 311  
Qy 614 GTTCCTGCGGAGCGGAGCCCTTGGACCCCTGATGAGCCCGACCTTCCATCCAGACGC 673  
Db 312 GTTCCTGCGGAGCGGAGCCCTTGGACCCCTGATGAGCCCGACCTTCCATCCAGACGC 371  
Qy 674 GAGCTGCTCGGAGGAACTTGTATCTTCAACGACAAAGAGGCTTTGCGACTGACTCGGC 733  
Db 372 GAGCTGCTCGGAGGAACTTGTATCTTCAACGACAAAGAGGCTTTGCGACTGACTCGGC 431  
Qy 734 CGTGCTCTGACACCTTCAGAGAGGAGGCTGCGCGCCGCTTCTGCTGCGGAGCCCGGAG 793  
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RESULT 14  
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LOCUS AGENCOURT 7049519 NIH\_MGC\_107 Homo sapiens cDNA clone IMAGE:5805370  
DEFINITION 5', mRNA sequence.  
ACCESSION BQ278726  
VERSION BQ278726.1 GI:20488934  
KEYWORDS EST.  
SOURCE  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 1043)  
NIH-MGC <http://mgi.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: ATCC  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1CM2044 row: h column: 11  
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Site:2: XhoI; cDNA made by oligo-dT priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 69.1%; Score 831.2; DB 5; Length 1043;  
Best Local Similarity 99.2%; Pred. No. 1.9e-215;  
Matches 877; Conservative 0; Mismatches 3; Indels 4; Gaps 4;  
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Qy 382 CCCGTTGGCGGCTCTACAGAGCGGTGCTGCTGCTGCGAAGCGAGCTGCGCATGCC 441  
Db 60 CCCGTTGGCGGCTCTACAGAGCGGTGCTGCTGCTGCGAAGCGAGCTGCGCATGCC 119  
Qy 442 CCGGGGCGGAGGAGCGCGGCGAGCTGAGAGCGGCTGAGCTTGTGAGCATGAA 501  
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Qy 502 CCACTGCTACTCCGCTGCGGAACTGTATCCGAGAGTCCGAGAGGCACTCACTTAG 561  
Db 180 CCACTGCTACTCCGCTGCGGAACTGTATCCGAGAGTCCGAGAGGCACTCACTTAG 239  
Qy 562 CCAAGTGAATCTTACAGCGGCTATGATGATCACTTCTGACCTGCAAGTATGCTGGC 621  
Db 240 CCAAGTGAATCTTACAGCGGCTATGATGATCACTTCTGACCTGCAAGTATGCTGGC 299  
Qy 622 CGAGCGAGCGGCTGAGCGGCTGATGAGCGGCGGCACTTCCATCCAGAGCGGAGCTGC 681  
Db 300 CGAGCGAGCGGCTGAGCGGCTGATGAGCGGCGGCACTTCCATCCAGAGCGGAGCTGC 359  
Qy 682 TCCGGAATTTGATCTCCAGAGCAAGAGAGCTTTTGCACGTGAGCTGAGCGGTCTCT 741  
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QY	981	CCCAAGTCTAAGGCTCTTTTCAGACGCTGAGGCTGTGGAGAGTGCGCTCTCCAAAC	1040
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QY	1041	TATGCGAAGCGCGCGCACAGCTGGTCTGTGCTCCCTGGAGAAAGTTCTGTGCCC	1100
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RESULT 15	AL551330	LOCUS	DEFINITION
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ACCESSION AL551330  
VERSION AL551330.3 GI:45856137

SOURCE ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE  
Mammalia; Eutheria; Primates; Catarrhini; Hominae; Homo.  
1 (pages 1 to 999)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Bryozoa; Mollusca; Echinodermata; Cephalopoda

**AUTHORS** Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
**TITLE** Full-length cDNA libraries and normalization  
**JOURNAL** Unpublished (2001)  
**COMMENT**

COMMENT: On Feb 15, 2001 this sequence replaced gi:31273146.

Genoscope - Centre National de Séquençage  
RD 161 0100 Evry Cedex France

Email: [seget@genoscope.cns.fr](mailto:seget@genoscope.cns.fr), Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five primers  
and enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
set 1.

For more information about this cluster, see <http://www.genoscope.cns.fr/cda?c=CS0D1064BD06QPI&c=951.r>

## FEATURES

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/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

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## ORIGIN

Query Match	Score	DB	Length
69.0%	830	1	898

Matches 863; Conservative 2; Mismatches 2; Indels 3; Gaps 3;

336 TCTTTGGGCACCTCTGACTACTCCCGAGCATGAAGCGCTGAGCCCGGTCCGCGCT 395

Db 1 TCTTTGGGCACTCTGACTCACTCCCGAGCATGAAGCGCTGAGCCCGGTGCGCGCT 60

396 GCTACGAGCGGTGTGCTGCTGTCGGAACGCACTTGCCATCGCCCGGGCCGAGGA 455

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456 AGGGCCCGCAGCTGAGGAGCCGCTGAGCTTCTGGACGACATGAACCACTGCTACTCCC 515

Db 121 AGGGCCCGCAGCTGAGGAGCCGCTGAGCTTGCTGGACGACATGAAACCACTGTA

516 GCTTCGGACCTGGTACCCGGAGTCCCGAGAGGCACTCAGCTTAGCCAGGTGGAATCC 575

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1. *Chlorophyll a* (Chl *a*)

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[illegible]

Db 361 TCTCAACGACAAAGGAGCTTTGGCACTGACTGGCCGTCTCTGACACCTTCAGAAC 420

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Search completed: December 18, 2004, 20:21:53  
Job time : 4385.17 secs